STIC-Biotech/ChemLib

71084 CRFF

Fr m: Schmidt, Mary
Sent: Tuesday, July 16, 2002 4:42 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request 09/716,320

please search seq id no. 3-- this is a short antisense sequence, so please size limit the results to less than 100 bases.
please include an interference search also.

thanks,
melissa
au 1635
11e12 mailboxes

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

seq-3 (15 residues)

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 7/18/02
Date Completed: 7/22/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 06
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 20, 2002, 22:43:05 ; Search time 1800.28 Seconds
(without alignments)
174.361 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 843946

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	19	6	AX103821	AX103821 Sequence
	2	15	100.0	19	6	AX355038	AX355038 Sequence
c	3	15	100.0	24	6	I34918	I34918 Sequence 4
	4	14	93.3	15	6	AR071406	AR071406 Sequence
	5	14	93.3	51	6	AX159179	AX159179 Sequence
	6	13	86.7	14	6	A45228	A45228 Sequence 10
	7	13	86.7	14	6	A88989	A88989 Sequence 11
	8	13	86.7	16	6	A88177	A88177 Sequence 32
	9	13	86.7	16	6	A90144	A90144 Sequence 32
	10	13	86.7	20	6	AR137074	AR137074 Sequence
c	11	13	86.7	20	6	AX164704	AX164704 Sequence
	12	13	86.7	26	6	AR122156	AR122156 Sequence
	13	13	86.7	26	6	AR142598	AR142598 Sequence
c	14	12.4	82.7	22	6	AR054584	AR054584 Sequence
c	15	12.4	82.7	50	6	AX161043	AX161043 Sequence
	16	12.4	82.7	51	6	AX159180	AX159180 Sequence
c	17	12.4	82.7	51	6	AX161039	AX161039 Sequence
c	18	12.4	82.7	51	6	AX161040	AX161040 Sequence
c	19	12.4	82.7	51	6	AX161041	AX161041 Sequence
c	20	12	80.0	22	6	E15265	E15265 Primer. 7/1
c	21	12	80.0	27	6	AR017897	AR017897 Sequence
c	22	12	80.0	53	6	AR017882	AR017882 Sequence
c	23	12	80.0	62	6	AR017883	AR017883 Sequence
	24	12	80.0	97	6	E15263	E15263 Chlamydomon
	25	11.8	78.7	50	6	AR077265	AR077265 Sequence
	26	11.8	78.7	50	6	AX199506	AX199506 Sequence
	27	11.8	78.7	51	6	AX199505	AX199505 Sequence
c	28	11.8	78.7	64	6	AR048884	AR048884 Sequence
	29	11.8	78.7	72	9	AF159095	AF159095 Homo sapi
c	30	11.8	78.7	93	9	AF172205	AF172205 Nycticebu
c	31	11.8	78.7	93	9	AF172208	AF172208 Eulemur m
c	32	11.8	78.7	93	9	AF172209	AF172209 Perodicti
	33	11.8	78.7	96	3	CELE11937	AJ011937 Caenorhab
	34	11.8	78.7	100	6	AR048314	AR048314 Sequence
	35	11.8	78.7	100	6	AR097085	AR097085 Sequence
	36	11.8	78.7	100	6	AR130583	AR130583 Sequence
	37	11.8	78.7	100	6	AR171932	AR171932 Sequence
	38	11.4	76.0	20	6	AR136387	AR136387 Sequence
c	39	11.4	76.0	20	6	E28760	E28760 Antitumor d
	40	11.4	76.0	25	6	A03718	A03718 Oligonucleo
c	41	11.4	76.0	35	6	E16642	E16642 PCR primer
c	42	11.4	76.0	35	6	E27315	E27315 DNA synthas
	43	11.4	76.0	40	6	A03719	A03719 Oligonucleo
	44	11.4	76.0	42	6	AX128374	AX128374 Sequence
c	45	11.4	76.0	48	6	AX232549	AX232549 Sequence

ALIGNMENTS

RESULT 1
AX103821
LOCUS AX103821 19 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 13 from Patent WO0122972.
ACCESSION AX103821
VERSION AX103821.1 GI:13920018
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 19)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 13 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
source 1. .19
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BASE COUNT 3 a 6 c 5 g 5 t
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Db      4 TCCATGGTGCTCACT 18


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LOCUS       AX355038                  19 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 66 from Patent WO0197843.
ACCESSION   AX355038
VERSION     AX355038.1  GI:18619705
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (sites)
  AUTHORS   Weiner,G. and Hartmann,G.
  TITLE     Methods for enhancing antibody-induced cell lysis and treating
            cancer
  JOURNAL   Patent: WO 0197843-A 66 27-DEC-2001;
            UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES             Location/Qualifiers
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BASE COUNT        3 a      6 c      5 g      5 t
ORIGIN


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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
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Db      4 TCCATGGTGCTCACT 18


RESULT   3
I34918/c
LOCUS       I34918                    24 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 4 from patent US 5599704.
ACCESSION   I34918
VERSION     I34918.1  GI:2087886
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Thompson,J.D. and Draper,K.G.
  TITLE     ErbB2/neu targeted ribozymes
  JOURNAL   Patent: US 5599704-A 4 04-FEB-1997;
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Db     21 TCCATGGTGCTCACT 7


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LOCUS       AR071406                  15 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 1 from patent US 5910583.
ACCESSION   AR071406
VERSION     AR071406.1  GI:7222294
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Marks,J.R., Vaughn,J.P. and Inglehart,J.D.
  TITLE     Antisense oligonucleotides against ERBB-2
  JOURNAL   Patent: US 5910583-A 1 08-JUN-1999;
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  Query Match             93.3%;  Score 14;  DB 6;  Length 15;
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Qy      1 tccatggtgctcac 14
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Db      2 TCCATGGTGCTCAC 15


RESULT   5
AX159179
LOCUS       AX159179                  51 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2507 from Patent WO0140521.
ACCESSION   AX159179
VERSION     AX159179.1  GI:14540510
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 51)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 2507 07-JUN-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /note="1 of 2 allelic variants (2508 is other entry)
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Db     17 CCATGGTGCTCACT 30


RESULT   6
A45228
LOCUS       A45228                    14 bp    DNA     linear   PAT 07-MAR-1997
DEFINITION  Sequence 105 from Patent WO9517507.
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ACCESSION   A45228
VERSION     A45228.1  GI:2299723
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W., Schlingensiepen,K., Schlingensiepen,R. and
            Schlingensiepen,G.
  TITLE     ANTISENSE NUCLEIC ACIDS FOR THE PREVENTION AND TREATMENT OF
            DISORDERS IN WHICH EXPRESSION OF c-erbB PLAYS A ROLE
  JOURNAL   Patent: WO 9517507-A 105 29-JUN-1995;
            BIOGNOSTIK GES (DE)
COMMENT     Other publication AU 1313095 950710.
FEATURES             Location/Qualifiers
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 catggtgctcact 15
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Db      1 CATGGTGCTCACT 13


RESULT   7
A88989
LOCUS       A88989                    14 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 1137 from Patent WO9833904.
ACCESSION   A88989
VERSION     A88989.1  GI:6737559
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 1137 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES             Location/Qualifiers
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Qy      3 catggtgctcact 15
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Db      1 CATGGTGCTCACT 13


RESULT   8
A88177
LOCUS       A88177                    16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 325 from Patent WO9833904.
ACCESSION   A88177
VERSION     A88177.1  GI:6736747
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W. and Schlingensiepen,K.
  TITLE     AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
  JOURNAL   Patent: WO 9833904-A 325 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
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BASE COUNT        2 a      5 c      5 g      4 t
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  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 catggtgctcact 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT   9
A90144
LOCUS       A90144                    16 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 325 from Patent EP0856579.
ACCESSION   A90144
VERSION     A90144.1  GI:6738658
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Brysch,W.D. and Schlingensiepen,K.D.
  TITLE     An antisense oligonucleotide preparation method
  JOURNAL   Patent: EP 0856579-A 325 05-AUG-1998;
            BIOGNOSTIK GES (DE)
FEATURES             Location/Qualifiers
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Qy      3 catggtgctcact 15
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Db      1 CATGGTGCTCACT 13


RESULT  10
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LOCUS       AR137074                  20 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 3 from patent US 6162965.
ACCESSION   AR137074
VERSION     AR137074.1  GI:14478324
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Hansen,G.
  TITLE     Plant transformation methods
  JOURNAL   Patent: US 6162965-A 3 19-DEC-2000;
FEATURES             Location/Qualifiers
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BASE COUNT        4 a      4 c      7 g      5 t
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Qy      1 tccatggtgctca 13
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Db      6 TCCATGGTGCTCA 18


RESULT  11
AX164704/c
LOCUS       AX164704                  20 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 9 from Patent WO0136644.
ACCESSION   AX164704
VERSION     AX164704.1  GI:14545596
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequence.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Rastelli,L., Lewin,D., Taillon,B. and Andrew,D.P.
  TITLE     Wnt-regulated cytokine-like polypeptide and nucleic acids encoding
            same
  JOURNAL   Patent: WO 0136644-A 9 25-MAY-2001;
            Curagen Corporation (US)
FEATURES             Location/Qualifiers
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Db     20 CATGGTGCTCACT 8


RESULT  12
AR122156
LOCUS       AR122156                  26 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 18 from patent US 6165712.
ACCESSION   AR122156
VERSION     AR122156.1  GI:14106473
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Foulkes,J.Gordon, Leichtfried,F.E., Pieler,C., Stephenson,J.R. and
            Case,C.C.
  TITLE     Methods of transcriptionally modulating expression of viral genes
            and genes useful for production of proteins
  JOURNAL   Patent: US 6165712-A 18 26-DEC-2000;
FEATURES             Location/Qualifiers
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Qy      3 catggtgctcact 15
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Db      1 CATGGTGCTCACT 13


RESULT  13
AR142598
LOCUS       AR142598                  26 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 6 from patent US 6203976.
ACCESSION   AR142598
VERSION     AR142598.1  GI:15103884
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 26)
  AUTHORS   Foulkes,J.Gordon, Leichtfried,F.E., Pieler,C. and Stephenson,J.R.
  TITLE     Methods of preparing compositions comprising chemicals capable of
            transcriptional modulation
  JOURNAL   Patent: US 6203976-A 6 20-MAR-2001;
FEATURES             Location/Qualifiers
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Db      1 CATGGTGCTCACT 13


RESULT  14
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LOCUS       AR054584                  22 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5837447.
ACCESSION   AR054584
VERSION     AR054584.1  GI:5980161
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Gorski,J.
  TITLE     Monitoring an immune response by analysis of amplified
            immunoglobulin or T-cell-receptor nucleic acid
  JOURNAL   Patent: US 5837447-A 5 17-NOV-1998;
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LOCUS       AX161043                  50 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4371 from Patent WO0140521.
ACCESSION   AX161043
VERSION     AX161043.1  GI:14542374
KEYWORDS    .
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SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 50)
  AUTHORS   Shimkets,R.A. and Leach,M.
  TITLE     Nucleic acids containing single nucleotide polymorphisms and
            methods of use thereof
  JOURNAL   Patent: WO 0140521-A 4371 07-JUN-2001;
            Curagen Corporation (US)
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                     /note="1 of 2 allelic variants (4372 is other entry)"
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Job time: 18516 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 02:44:51 ; Search time 203.9 Seconds
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Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

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Listing first 45 summaries

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23: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	21	AAZ90403	Phosphorothioated
	2	15	100.0	19	22	AAF98894	Immunostimulatory
.c	3	15	100.0	24	14	AAQ52043	Breast cancer spec
c	4	15	100.0	70	20	AAX80767	Promoter region of
	5	14	93.3	15	19	AAV40434	US-1 antisense oli
	6	14	93.3	51	22	AAI75566	Human silent SNP c
c	7	13.4	89.3	24	19	AAV22685	PCR primer HN40 us
c	8	13.4	89.3	29	22	AAS09199	PCR primer #1 used
	9	13	86.7	14	16	AAQ92762	c-erbB-2 antisense
	10	13	86.7	16	19	AAV48736	ErbB-2 gene antise
c	11	13	86.7	19	21	AAA53776	Forward primer for
c	12	13	86.7	19	22	AAD15845	Human HER-2 ECD co
	13	13	86.7	20	20	AAV84090	PCR primer MTL(P)
c	14	13	86.7	20	22	AAS00677	Human consensus se
	15	13	86.7	20	22	AAF26607	Maize metallothion
	16	12.4	82.7	20	21	AAA74062	Reverse PCR primer
c	17	12.4	82.7	22	20	AAV08115	Primer Vbeta5 for
	18	12.4	82.7	47	20	AAZ01091	Probe for human PG
c	19	12.4	82.7	50	22	AAI77430	Human silent SNP c
	20	12.4	82.7	51	22	AAI75567	Human silent SNP c
c	21	12.4	82.7	51	22	AAI77426	Human silent SNP c
c	22	12.4	82.7	51	22	AAI77427	Human silent SNP c
c	23	12.4	82.7	51	22	AAI77428	Human silent SNP c
c	24	12	80.0	22	19	AAV17078	Oligonucleotide 6
c	25	12	80.0	27	19	AAV36673	Nucleotide sequenc
c	26	12	80.0	53	19	AAV36662	Nucleotide sequenc
c	27	12	80.0	62	19	AAV36663	Nucleotide sequenc
	28	12	80.0	97	19	AAV17076	Oligonucleotide 4
	29	11.8	78.7	20	21	AAA12081	Human ICAM-1 antis
c	30	11.8	78.7	22	21	AAA52945	Mouse EphA4 gene P
	31	11.8	78.7	32	21	AAA52982	HCV-1a E2 forward
c	32	11.8	78.7	42	21	AAA12095	Human ICAM-1 DNA f
	33	11.8	78.7	50	18	AAT89212	Prostate specific
	34	11.8	78.7	50	22	AAH89655	Human kinase codin
c	35	11.8	78.7	51	21	AAA76472	Membrane transport
c	36	11.8	78.7	51	21	AAA76473	Membrane transport
	37	11.8	78.7	51	22	AAH89654	Human kinase codin
c	38	11.8	78.7	54	17	AAT50594	Human CETP hairpin
c	39	11.8	78.7	54	18	AAX71673	Human KDR VEGF rec
	40	11.8	78.7	100	19	AAV59359	Nucleotide sequenc
	41	11.8	78.7	100	21	AAA12495	cDNA encoding a co
c	42	11.6	77.3	39	21	AAA40195	H. pylori immunogl
c	43	11.6	77.3	39	21	AAA40196	H. pylori immunogl
c	44	11.6	77.3	39	22	AAF88090	H. pylori derived
c	45	11.6	77.3	39	22	AAF88091	H. pylori derived

ALIGNMENTS

RESULT 1
AAZ90403
ID AAZ90403 standard; DNA; 15 BP.
XX
AC AAZ90403;
XX
DT 30-MAY-2000 (first entry)
XX
DE Phosphorothioated ASO directed against HER-2 gene.
XX
KW Radiation; drug resistance; HER-2; raf-1; radioresistant; tumour;
KW cancer; restenosis; osteoarthritis; neurological; pre-eclampsia;
KW intestinal abnormality; antisense; ss.
XX
OS Homo sapiens.
XX
PN US6027892-A.
XX
PD 22-FEB-2000.
XX
PF 16-DEC-1997; 97US-0991830.
XX
PR 30-DEC-1996; 96US-0034160.
XX
PA (CHAN/) CHANG E H.
PA (PIRO/) PIROLLO K F.
XX
PI Chang EH, Pirollo KF;
XX
DR WPI; 2000-194828/17.
XX
PT Reducing radiation or drug resistance in a cell comprises introduction

PT of antisense nucleic acid for treating or diagnosing cancer,
PT restenosis, osteoarthritis, neurological and intestinal abnormalities
PT and pre-eclampsia -
XX
PS Claim 4; Column 9; 18pp; English.
XX
CC The invention provides a method for reducing radiation or drug resistance
CC of a cell, in vitro, which does not overexpress HER-2 or raf-1 genes.
CC The method comprises introducing to the cell an antisense nucleic acid
CC comprising a segment complementary to HER-2 or raf-1. The method is
CC useful for increasing drug and radiation sensitivity in a cell,
CC particularly in the treatment of radioresistant tumours. The antisense
CC nucleic acids are useful for treating or diagnosing cancer, restenosis,
CC osteoarthritis, neurological and intestinal abnormalities and
CC pre-eclampsia. The present sequence represents a phosphorothioated
CC antisense oligo (ASO) directed against HER-2 gene.
XX
SQ Sequence 15 BP; 2 A; 5 C; 3 G; 5 T; 0 other;

Query Match 100.0%; Score 15; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctcact 15
||||||||||||||||
Db 1 tccatggtgctcact 15

RESULT 2
AAF98894
ID AAF98894 standard; DNA; 19 BP.
XX
AC AAF98894;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #10.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US26383.
XX
PR 25-SEP-1999; 99US-0156113.
PR 27-SEP-1999; 99US-0156135.
PR 23-AUG-2000; 2000US-0227436.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids -
XX
PS Disclosure; Page 38; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells.
CC Note: the present sequence may have a phosphorothioate backbone.
XX
SQ Sequence 19 BP; 3 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctcact 15
||||||||||||||||
Db 4 tccatggtgctcact 18

RESULT 3
AAQ52043/c
ID AAQ52043 standard; RNA; 24 BP.
XX
AC AAQ52043;
XX
DT 26-MAY-1994 (first entry)
XX
DE Breast cancer specific mRNA ribozyme cleavable nucleotide (159).
XX
KW Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
OS Homo sapiens.
XX
PN WO9323057-A.
XX
PD 25-NOV-1993.
XX
PF 13-MAY-1993; 93WO-US04573.
XX
PR 14-MAY-1992; 92US-0882822.
PR 14-MAY-1992; 92US-0882885.
PR 26-AUG-1992; 92US-0936110.
PR 26-AUG-1992; 92US-0936421.
PR 26-AUG-1992; 92US-0936422.
PR 26-AUG-1992; 92US-0936531.
PR 26-AUG-1992; 92US-0936532.
PR 07-DEC-1992; 92US-0987131.
PR 19-JAN-1993; 93US-0006122.
PR 19-JAN-1993; 93US-0008910.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Draper KG, Thompson JD;
XX
DR WPI; 1993-386203/48.
XX
PT New enzymatic RNA molecules (ribozymes) - which cleave mRNA
PT associated with tumours or mRNA expressed from gene encoding
PT multiple drug resistance
XX
PS Claim 3; Fig 8; 69pp; English.
XX
CC The sequences given in AAQ51825-2266 represent areas of mRNAs which are

CC associated with development or maintenance of chronic myelogenous
CC leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or
CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
CC and lung cancer. The full length mRNAs containing these target
CC sequences, encode aberant cellular proteins which are able to control
CC cellular proliferation and are directly linked to a leukemic
CC phenotype. These target sequences are identified by the ribozyme of
CC the invention. The ribozymes is formed in a hammerhead motif, but may
CC also be formed in the motif of a hairpin, hepatitis delta virus, group
CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
CC the development or expression of a transformed phenotype in man and
CC other animals by modulating expression of the corresponding gene.
CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed
CC cells elicits inhibition of the transformed state. Multiple drug
CC resistance (mdr-1) mRNA specific ribozymes remove the mechanism of
CC drug resistance used by transformed cells and thus enhances drug
CC therapies for tumours. The ribozymes may also be used to study
CC genetic drift and mutations within cells.
XX
SQ Sequence 24 BP; 6 A; 7 C; 8 G; 3 U; 0 other;

Query Match 100.0%; Score 15; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctcact 15
||||||||||||||||
Db 21 TCCATGGTGCTCACT 7

RESULT 4
AAX80767/c
ID AAX80767 standard; DNA; 70 BP.
XX
AC AAX80767;
XX
DT 26-OCT-1999 (first entry)
XX
DE Promoter region of HER-2 DNA target sequence.
XX
KW HER-2; c-erb-B2; target sequence; antisense molecule; HERMYC1; HERMYC2;
KW HERMYC1R; HERMYC2R; breast cancer; c-myc; promoter region; HER 5';
KW topological linkage; padlock DNA; malignancy; metastasis; tumour;
KW transcription factors; gene therapy; cultured cell; amplification;
KW antisense technology; therapeutic modulation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_binding 6..20
FT /*tag= a
FT /bound_moiety= "HERMYC1 or HERMYC1R antisense molecule"
FT /note= "Forms a duplex in the presence of HERMYC1 in
FT AAX80768 or HERMYC1R antisense molecule in AAX80770"
FT misc_binding 37..50
FT /*tag= b
FT /bound_moiety= "HERMYC2 or HERMYC2R antisense molecule"
FT /note= "Forms a duplex in the presence of HERMYC2 in
FT AAX80769 or HERMYC2R antisense molecule in AAX80771"
XX
PN WO9909045-A1.
XX
PD 25-FEB-1999.
XX
PF 20-AUG-1998; 98WO-US17268.
XX
PR 20-AUG-1997; 97US-0056742.
XX
PA (SOMA-) SOMAGENICS INC.
XX
PI Johnston BH, Kazakov SA, Kisich KO;
XX
DR WPI; 1999-228889/19.
XX
PT A new antisense molecule which topologically links to target mRNA
XX
PS Example 5; Fig 8; 134pp; English.
XX
CC The present sequence is the 5'promoter region of HER-2 oncogene, that
CC undergoes genetic alterations along with c-myc gene and is associated
CC with aggressive breast cancer and poor prognosis. Overexpression of
CC HER-2 gene has been shown to enhance malignancy and metastasis.
CC Repression of HER-2 in mouse tumours leads to suppression of tumour
CC growth and longer life of the animal. This can be done by using padlock
CC DNAs, HERMYC1, HERMYC1R, HERMYC2 and HERMYC2R, that target a G rich
CC sequence in the promoter region. It inhibits binding of transcription
CC factors. This sequence can be used as a target sequence in antisense
CC technology for therapeutic modulation of gene expression in cultured
CC cells and whole animals, for gene function analysis and target
CC validation for gene therapy and for the detection and amplification of
CC nucleic acids.
XX
SQ Sequence 70 BP; 6 A; 25 C; 26 G; 13 T; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 70;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctcact 15
||||||||||||||||
Db 28 TCCATGGTGCTCACT 14

RESULT 5
AAV40434
ID AAV40434 standard; DNA; 15 BP.
XX
AC AAV40434;
XX
DT 28-SEP-1998 (first entry)
XX
DE US-1 antisense oligonucleotide used to down regulate ERBB2 oncogene.
XX
KW Antisense oligonucleotide; down regulate; erbB-2; oncogene;
KW tyrosine kinase; breast cancer; radioisotope; hybridisation; probe;
KW US-1; US-3; US-4; US-5; UT-1; US-D; SC-3; TRACER; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9820168-A1.
XX
PD 14-MAY-1998.
XX
PF 03-NOV-1997; 97WO-US20910.
XX
PR 04-NOV-1996; 96US-0740821.
XX
PA (UYDU-) UNIV DUKE.
XX
PI Inglehart JD, Marks JR, Vaughn JP;
XX
DR WPI; 1998-286977/25.
XX
PT Antisense oligonucleotides that down regulate the erbB-2 oncogene -
PT useful to inhibit ERBB2 tyrosine kinase receptor expression in
PT cancer cells to treat epithelial cell, breast, ovarian, lung or
PT colon cancer
XX
PS Example 6; Page 15; 31pp; English.
XX
CC The antisense oligonucleotides AAV40432-V40439 were used to down
CC regulate the erbB-2 oncogene. This oncogene codes for a 185kD tyrosine

CC kinase linked transmembrane protein which in 30-50% of primary breast
CC cancers is overexpressed. The oligonucleotides are able to inhibit the
CC overexpression of ERBB2 tyrosine kinase receptor in a cell, which can be
CC done by targeting the antisense oligonucleotides to the erbB-2 oncogene.
CC By labelling the oligonucleotides with, for example, a radioisotope,
CC they can also be used as hybridisation probes to detect the ERBB2 gene.
CC The oligonucleotides were designated the following names, followed by
CC the location in the erbB-2 gene that they target: US-1 (166-180); US-3
CC (160-174); US-4 (173-187); US-5 (178-192); UT-1 (151-165); US-D
CC (US-1 scrambled control); SC-3 (US-3 scrambled control); TRACER
CC (fluoresceinated tracer). It was found that all of the oligonucleotides
CC (apart from the controls) inhibited the erbB-2 protein, however with
CC varying degrees of effectiveness. US-3 and UT-1 were identified as
CC being the most efficient oligonucleotides at inhibiting erbB-2. The
CC oligonucleotides are useful in vivo to treat cancer (especially
CC epithelial cell, breast, ovarian, lung or colon cancer) in a human or
CC other animal, especially when the cancer is characterised by cells that
CC overexpress the ERBB2 tyrosine kinase receptor.
XX
SQ Sequence 15 BP; 2 A; 6 C; 3 G; 4 T; 0 other;

Query Match 93.3%; Score 14; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctcac 14
||||||||||||||
Db 2 tccatggtgctcac 15

RESULT 6
AAI75566
ID AAI75566 standard; DNA; 51 BP.
XX
AC AAI75566;
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:2507.
XX
KW Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
PN WO200140521-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32758.
XX
PR 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-356160/37.
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
PS Claim 1; Page 818; 2653pp; English.
XX
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 7 A; 14 C; 15 G; 15 T; 0 other;

Query Match 93.3%; Score 14; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ccatggtgctcact 15
||||||||||||||
Db 17 ccatggtgctcact 30

RESULT 7
AAV22685/c
ID AAV22685 standard; DNA; 24 BP.
XX
AC AAV22685;
XX
DT 20-JUL-1998 (first entry)
XX
DE PCR primer HN40 used to amplify ErbB-2.
XX
KW ErbB-2 protein; vaccine; T-cell damage; activation; T-cell; treatment;
KW prevention; viral disease; cancer; autoimmune disorder; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9809650-A1.
XX
PD 12-MAR-1998.
XX
PF 05-SEP-1997; 97WO-JP03123.
XX
PR 06-SEP-1996; 96JP-0236937.
XX
PA (MITU) MITSUBISHI CHEM CORP.
XX
PI Nakamura H, Shiku H, Sunamoto J;
XX
DR WPI; 1998-193326/17.
XX
PT Vaccine preparation comprises antigen and hydrophobic polysaccharide
PT - e.g. mannan containing sterol groups for treating, e.g. cancer
XX
PS Example 1; Page 9; 27pp; English.
XX
CC PCR primers AAV22685-86 are used to amplify DNA encoding ErbB-2
CC proteins. The specification describes a vaccine preparation that
CC comprises an antigen and, optionally, a hydrophobic polysaccharide (HPS)
CC optionally as a composite. The antigen is a protein, such as ErbB-2 class
CC 1-9 proteins, which initiate T-cell damage. The vaccine activates T-cells
CC and is useful for the treatment and prevention of viral diseases, cancer
CC and autoimmune disorders.
XX
SQ Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;

Query Match 89.3%; Score 13.4; DB 19; Length 24;
Best Local Similarity 93.3%; Pred. No. 4.5e+02;

```
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
           ||||||||| |||||
Db      21 TCCATGGTGATCACT 7


RESULT   8
AAS09199/c
ID   AAS09199 standard; DNA; 29 BP.
XX
AC   AAS09199;
XX
DT   07-NOV-2001  (first entry)
XX
DE   PCR primer #1 used to amplify cDNA encoding murine CCR7.
XX
KW   Cell fusion assay; fluorescence resonance energy transfer; FRET;
KW   beta-lactamase; inhibition of cell fusion; CD4; cytokine receptor;
KW   viral disease; HIV-1 infection; mouse; murine; CCR7; Th1 cell;
KW   PCR primer; ss.
XX
OS   Mus sp.
XX
PN   WO200160995-A1.
XX
PD   23-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-US04677.
XX
PR   17-FEB-2000; 2000US-0183309.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Sullivan KA,  Benincasa D,  Cascieri MA,  Mitnaul LJ,  Shiao L;
PI   Tota MR;
XX
DR   WPI; 2001-536569/59.
XX
PT   Determining the amount of fusion that occur between two cells comprises
PT   measurement of fluorescence energy transfer -
XX
PS   Disclosure; Page 14; 59pp; English.
XX
CC   The present invention relates to a method for determining the amount
CC   of fusion that occurs between two cells, one of which contains the
CC   enzyme beta-lactamase and the other of which contains a fluorescent
CC   substrate of beta-lactamase. The method comprises the measurement of
CC   fluorescence resonance energy transfer (FRET). The invention also
CC   provides methods of identifying inhibitors of the fusion of two
CC   types of cells, particularly when fusion is mediated by the
CC   interaction of a viral protein and target cellular proteins e.g. CD4
CC   and cytokine receptors. The methods are useful for identifying
CC   substances that are useful for the treatment of viral diseases,
CC   particularly for the identification of inhibitors of HIV-1 infection.
CC   The present sequence for PCR primer #1 is used with PCR primer #2
CC   (AAS09200) to amplify cDNA encoding CCR7 from murine Th1 cells.
XX
SQ   Sequence 29 BP; 9 A; 8 C; 10 G; 2 T; 0 other;


  Query Match             89.3%;  Score 13.4;  DB 22;  Length 29;
  Best Local Similarity   93.3%;  Pred. No. 4.6e+02;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
           |||||||||||| ||
Db      23 TCCATGGTGCTCTCT 9


RESULT   9
AAQ92762
ID   AAQ92762 standard; DNA; 14 BP.
XX
AC   AAQ92762;
XX
DT   13-FEB-1996  (first entry)
XX
DE   c-erbB-2 antisense nucleic acid #105.
XX
KW   Antisense nucleic acid; c-erbB-2; inhibition; fibroblast; neoplasm;
KW   p185-erbB-2 protein tyrosine kinase; tumour; breast cancer; detection;
KW   immune disease; angiogenesis; ss.
XX
OS   Synthetic.
XX
PN   WO9517507-A1.
XX
PD   29-JUN-1995.
XX
PF   09-DEC-1994;  94WO-EP04094.
XX
PR   23-DEC-1993;  93EP-0120710.
XX
PA   (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI   Brysch W,  Schlingensiepen G,  Schlingensiepen K,  Schlingensiepen R;
XX
DR   WPI; 1995-240669/31.
XX
PT   New anti:sense nucleic acid against C-erbB-2 - for treating or
PT   preventing neoplasms, immune disease and angiogenesis, also for
PT   diagnosis
XX
PS   Claim 1; Page 48; 55pp; English.
XX
CC   The sequences given in AAQ92658-762 are antisense nucleic acids which
CC   hybridise with part of the mRNA and/or DNA encoding c-erbB-2.  These
CC   antisense nucleic acids are able to inhibit the expression of the
CC   p185-erbB-2 protein tyrosine kinase activity and cell growth in a
CC   number of tumour cells including breast cancer cells.  Untransformed
CC   normal fibroblasts are not growth inhibited by anti-c-erbB-2
CC   antisense compounds suggesting that p185-erbB-2 plays a pathogenic
CC   role in the growth of the above mentioned tumours.  These antisense
CC   oligonucleotides may be used in the prevention and treatment of
CC   neoplasms, immune diseases and/or diseases involving pathological
CC   angiogenesis when associated with c-erbB-2 expression.  They may also
CC   be used to detect expression of the relevant genes.
XX
SQ   Sequence 14 BP; 2 A; 4 C; 4 G; 4 T; 0 other;


  Query Match             86.7%;  Score 13;  DB 16;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 7.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 catggtgctcact 15
           |||||||||||||
Db       1 catggtgctcact 13


RESULT  10
AAV48736
ID   AAV48736 standard; DNA; 16 BP.
XX
AC   AAV48736;
XX
DT   15-OCT-1998  (first entry)
XX
DE   ErbB-2 gene antisense oligonucleotide ErbB-2-28.
XX
KW   ErbB-2; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
```

PN EP856579-A1.
XX
PD 05-AUG-1998.
XX
PF 31-JAN-1997; 97EP-0101531.
XX
PR 31-JAN-1997; 97EP-0101531.
XX
PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
PI Brysch W, Schlingensiepen K;
XX
DR WPI; 1998-400910/35.
XX
PT Preparation of antisense oligo:nucleotide(s) which lack long runs of
PT consecutive guanosine or inosine - and have specific ratio of
PT residues able to form two or three hydrogen bonds, have greater
PT activity and reduced toxicity, used therapeutically or to modulate
PT growth of cells in culture
XX
PS Claim 10; Fig 6a; 286pp; English.
XX
CC AAV48709-886 represent antisense oligonucleotides directed against the
CC ErbB-2 gene. Of these, only oligonucleotides AAV48709-91 resulted
CC in significant redcution in ErbB-2 protein expression, while
CC oligonucleotides AAV48792-886 had little effect. The oligonucleotides
CC exemplify the invention. The specification describes oligonucleotides
CC that contain 8-30 nucleotides, which contain at most 8 nucleotides that
CC can each form three hydrogen bonds to cytosine; do not contain four
CC consecutive nucleotides able to form three H-bonds each to four
CC consecutive cytosines; do not contain two sequences of three consecutive
CC nucleotides each able to form three H-bonds to three consecutive
CC cytosines, and the ratio between residues able to form two H-bonds each
CC (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The
CC oligonucleotides are used to modulate expression of genes, particularly
CC the genes for p53, ErB-2, junB, junD, TGF-beta 1 or beta 2 to control
CC proliferation of primary cell cultures (e.g. bone marrow stem, liver or
CC kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The
CC oligonucleotides can also be used to analyse function of proteins (by
CC altering their expression or activity) and therapeutically, e.g. in
CC cases of cancer or (targeting TGF) for stimulating the immune system.
XX
SQ Sequence 16 BP; 2 A; 5 C; 5 G; 4 T; 0 other;

Query Match 86.7%; Score 13; DB 19; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 catggtgctcact 15
||||||||||||||
Db 1 catggtgctcact 13

RESULT 11
AAA53776/c
ID AAA53776 standard; DNA; 19 BP.
XX
AC AAA53776;
XX
DT 04-DEC-2000 (first entry)
XX
DE Forward primer for HER-2 extracellular domain cDNA.
XX
KW HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion;
KW extracellular domain IIIa; antagonist; intron 8; C-terminal extension;
KW truncated HER-2; p68; dimerization inhibitor; cytostatic; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200044403-A1.
XX
PD 03-AUG-2000.
XX
PF 20-JAN-2000; 2000WO-US01484.
XX
PR 20-JAN-1999; 99US-0234208.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Doherty JK, Clinton GM, Adelman JP;
XX
DR WPI; 2000-499287/44.
XX
PT Using polypeptides and antibodies that bind to the extracellular domain
PT of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the
PT breast, lung, ovaries and colon
XX
PS Example 1; Page 14; 46pp; English.
XX
CC This primer, corresponding to HER-2 cDNA nucleotides 142-161, was used
CC to amplify the HER-2 extracellular domain. The reverse primers used are
CC shown in AAA53777 and AAA53778.
CC HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The
CC extracellular domain of p185-HER-2 is proteolytically shed from breast
CC carcinoma cells in culture and is found in serum of some cancer patients
CC and may be a serum marker of metastatic breast cancer. An alternative
CC HER-2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been
CC identified. The retained intron is in-frame and encodes a 79 amino acid
CC extension designated ECDIIIa (the present sequence), which is inserted at
CC residue 340 of p185-HER-2. The alternative mRNA predicts a truncated
CC HER-2 protein (approximately 68 kDa) that lacks the transmembrane and
CC intracellular domains (see AAY97240). p68HER-2 specifically binds to
CC p185-HER-2 without activating HER-2. It could therefore block
CC dimerization of p185-HER-2. The p68HER-2 polypeptide binds to a site on
CC the ECD of HER-2 that is different from the site of binding for
CC Herceptin (RTM) (a marketed humanized monoclonal antibody that is used
CC for the treatment of cancer and binds to the ECD of HER-2). The methods,
CC compositions, polypeptides and antibodies are used to treat solid
CC tumours such as breast cancer, small cell lung carcinoma, ovarian cancer
CC and/or colon cancer, especially where over-expression of HER-2 is
CC indicated.
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;

Query Match 86.7%; Score 13; DB 21; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctca 13
||||||||||||||
Db 13 TCCATGGTGCTCA 1

RESULT 12
AAD15845/c
ID AAD15845 standard; DNA; 19 BP.
XX
AC AAD15845;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human HER-2 ECD coding sequence amplifying forward PCR primer #1.
XX
KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; PCR primer;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200161356-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US05327.

XX
PR 16-FEB-2000; 2000US-0506079.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Clinton G, Henner WD, Evans A;
XX
DR WPI; 2001-529934/58.
XX
PT New polypeptide, which binds to the extracellular domain of HER-2 for
PT the treatment of hard tumors -
XX
PS Example 1; Page 22; 61pp; English.
XX
CC The invention relates to novel HER-2 (herstatin-2) antagonist
CC particularly a polypeptide that binds to the extracellular domain (ECD)
CC of HER-2 at a site that is different from the binding site of humanised
CC antibody, Herceptin, at an affinity of at least 10^8. The present
CC invention is based upon the initial discovery of an alternative HER-2
CC mRNA transcript with 274 bp insert of intron 8. The translation product
CC of the alternative transcript is a truncated HER-2 protein designated
CC p68HER-2 which lacks the transmembrane and intracellular domains of
CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIa.
CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
CC nucleic acids encoding these are useful to treat, diagnose and identify
CC solid tumours. The present sequence is a PCR primer used for amplifying
CC human HER2 ECD coding sequence.
XX
SQ Sequence 19 BP; 4 A; 5 C; 7 G; 3 T; 0 other;

Query Match 86.7%; Score 13; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctca 13
||||||||||||
Db 13 TCCATGGTGCTCA 1

RESULT 13
AAV84090
ID AAV84090 standard; DNA; 20 BP.
XX
AC AAV84090;
XX
DT 12-MAR-1999 (first entry)
XX
DE PCR primer MTL(P) used to amplify the iap, p35 and dad-1 genes.
XX
KW Transgenic maize; Agrobacterium induced necrosis inhibition;
KW metallothionein-like promoter; iap; p35; dad-1; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9854961-A2.
XX
PD 10-DEC-1998.
XX
PF 29-MAY-1998; 98WO-EP03215.
XX
PR 02-JUN-1997; 97US-0867869.
XX
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Hansen G;
XX
DR WPI; 1999-059863/05.
XX
PT Transforming plant cells using Agrobacterium - in conditions that
PT inhibit Agrobacterium-induced necrosis
XX
PS Example 8; Page 25; 47pp; English.
XX
CC PCR primers AAV84090-93 were used for the amplification and detection
CC of iap, p35 and dad-1 genes in transgenic maize callus, which was
CC transformed with these genes using the method of the invention. The
CC genes were cloned under the control of a metallothionein-like
CC promoter (MLP). PCR primer AAV84090 hybridises promoter sequences, and
CC is used in combination with each of the other primers in separate
CC reactions. The specification describes a new method for transforming a
CC plant cell with a gene of interest. The method comprises exposing the
CC cell to Agrobacterium carrying that gene, under conditions which inhibit
CC Agrobacterium induced necrosis (AIN). The method is used to transform
CC plants with a gene of interest.
XX
SQ Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 other;

Query Match 86.7%; Score 13; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctca 13
||||||||||||
Db 6 tccatggtgctca 18

RESULT 14
AAS00677/c
ID AAS00677 standard; DNA; 20 BP.
XX
AC AAS00677;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human consensus sequence 65677221-3-frag DNA probe.
XX
KW Wnt signalling pathway; FCTRX; cytokine-like polypeptide; human; cancer;
KW immune system disorder; tissue proliferation; neurological disorder; ss;
KW septic shock; arthritis; Crohn's disease; anaphylaxis; haemophilia; EST;
KW stroke; inflammatory bowel disease; depressive disorder; mammary tumour;
KW cognitive disorder; psoriasis; clone 7971c.7; expressed sequence tag;
KW consensus sequence 65677221-3-frag; probe.
XX
OS Homo sapiens.
XX
PN WO200136644-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US31629.
XX
PR 18-NOV-1999; 99US-0166177.
PR 16-NOV-2000; 2000US-0166177.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Rastelli L, Lewin D, Taillon B, Andrew DP;
XX
DR WPI; 2001-329224/34.
XX
PT S100 cytokine-like polypeptide member of the Wnt signalling pathway
PT designated (FCTRX) and the nucleic acid that encodes it, useful for
PT preventing, diagnosing and treating e.g. cancers and inflammation -
XX
PS Example 3; Page 86; 115pp; English.
XX
CC The sequence represents a DNA probe for expression analysis of human
CC consensus sequence 65677221-3-frag DNA which encompasses and extends the
CC human expressed sequence tag (EST) AA315020. AA315020 is similar to
CC murine clone 7971c.7 DNA which encodes a cytokine-like polypeptide member
CC of the Wnt signalling pathway and is expressed in murine mammary tumours.
CC Cytokine-like polypeptides and their associated polynucleotides are
CC termed FCTRX polypeptides and FCTRX polynucleotides. An alteration in the

CC amount of FCTRX protein can result in a pathology related to a
CC dysfunction in the immune system, a tissue proliferation-associated
CC disorder, or a neurological disorder. The sequences of the invention may
CC be used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate FCTRX expression, for example, by rectifying mutations
CC or deletions in a patient's genome that affect the activity of FCTRX by
CC expressing inactive proteins, or by supplementing the patients own
CC production of FCTRX. DNA molecules may be used to produce the FCTRX
CC protein by transforming a host cell and culturing the cell to express the
CC protein. Examples of disorders associated with abnormal FCTRX protein
CC expression include septic shock, arthritis, Crohn's disease, anaphylaxis,
CC stroke, haemophilia, cancer, inflammatory bowel disease, depressive
CC disorders, cognitive disorders, and psoriasis.
XX
SQ Sequence 20 BP; 7 A; 6 C; 5 G; 2 T; 0 other;

Query Match 86.7%; Score 13; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 catggtgctcact 15
||||||||||||||
Db 20 CATGGTGCTCACT 8

RESULT 15
AAF26607
ID AAF26607 standard; DNA; 20 BP.
XX
AC AAF26607;
XX
DT 27-MAR-2001 (first entry)
XX
DE Maize metallothionein-like gene promoter (MTL) PCR primer SEQ ID NO:3.
XX
KW Maize; Agrobacterium; transformation; plant; Gramineae; MTL;
KW metallothionein-like gene promoter; Agrobacterium induced necrosis;
KW inhibition; fertile; gramineceous plant; PCR primer; ss.
XX
OS Zea mays.
XX
PN US6162965-A.
XX
PD 19-DEC-2000.
XX
PF 02-JUN-1998; 98US-0089111.
XX
PR 02-JUN-1997; 97US-0098564.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Hansen G;
XX
DR WPI; 2001-090412/10.
XX
PT Agrobacterium transformation of gramineceous plants involves utilizing
PT Agrobacterium-induced necrosis inhibiting agents such as AIN inhibiting
PT nucleotide sequences or chemical compounds, or by heat shock treatment
PT -
XX
PS Example 8; Column 18; 19pp; English.
XX
CC The present invention describes a method (M1) for transforming a
CC gramineceous plant cell or tissue with a gene construct. The method
CC involves exposing the plant cell to Agrobacterium under conditions which
CC inhibit Agrobacterium induced necrosis (AIN) by the use of AIN inhibiting
CC agents such as chemical compounds, AIN inhibiting nucleotide sequences or
CC by heat shock treatment. Also described are: (1) a transgenic plant,
CC plant tissue or cell in whose genome a stably integrated nucleotide
CC sequence of heterologous origin which comprises a coding sequence of p35,
CC iap or dad-1 gene is present; and (2) a gramineceous plant cell or tissue
CC culture medium comprising an ethylene inhibitor other than silver nitrate
CC or an ethylene synthesis inhibitor and an Agrobacterium comprising a
CC plasmid which has a gene construct. (M1) is useful for producing a
CC fertile transgenic plant, preferably a gramineceous plant, e.g. maize
CC comprising a gene construct. The method involves transforming the plant
CC cell or tissue by exposing the plant cell or tissue to Agrobacterium
CC under conditions which inhibit AIN such as heat shocking, AIN inhibiting
CC nucleotide sequences stably integrated or transiently expressed or by use
CC of chemical inhibitors, and then regenerating the transformed plant cell
CC or tissue to produce the fertile transgenic plant. The fertile transgenic
CC maize plants comprise a genome having a stably integrated nucleotide
CC sequence of heterologous origin comprising a coding sequence of p35, iap
CC or dad-1 gene. The coding sequences preferably comprise maize preferred
CC codons. The present sequence represents a PCR primer which is used in an
CC example from the present invention.
XX
SQ Sequence 20 BP; 4 A; 4 C; 7 G; 5 T; 0 other;

Query Match 86.7%; Score 13; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctca 13
||||||||||||||
Db 6 tccatggtgctca 18

Search completed: July 21, 2002, 03:56:31
Job time: 4300 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 20, 2002, 22:56:25 ; Search time 43.28 Seconds
(without alignments)
85.132 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 613726

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	15	100.0	15	3	US-08-991-830A-3	Sequence 3, Appli
c	2	15	100.0	24	1	US-08-435-350-4	Sequence 4, Appli
	3	14	93.3	15	2	US-08-740-821-1	Sequence 1, Appli
	4	13	86.7	20	4	US-09-089-111-3	Sequence 3, Appli
	5	13	86.7	26	4	US-08-463-691-18	Sequence 18, Appl
	6	13	86.7	26	4	US-08-255-236-6	Sequence 6, Appli
c	7	12.4	82.7	22	2	US-08-229-528-5	Sequence 5, Appli
	8	12.4	82.7	47	4	US-09-338-907-248	Sequence 248, App
	9	12.4	82.7	47	4	US-09-218-207-248	Sequence 248, App
c	10	12	80.0	27	1	US-08-503-730-44	Sequence 44, Appl
c	11	12	80.0	53	1	US-08-503-730-29	Sequence 29, Appl
c	12	12	80.0	62	1	US-08-503-730-30	Sequence 30, Appl
	13	11.8	78.7	50	2	US-08-832-468-6	Sequence 6, Appli
c	14	11.8	78.7	54	1	US-08-363-240A-1077	Sequence 1077, Ap
c	15	11.8	78.7	54	4	US-08-584-040-4423	Sequence 4423, Ap
c	16	11.8	78.7	64	1	US-08-290-592E-41	Sequence 41, Appl
c	17	11.8	78.7	64	5	PCT-US96-09448-41	Sequence 41, Appl
	18	11.8	78.7	100	1	US-08-655-086-3	Sequence 3, Appli
	19	11.8	78.7	100	3	US-08-441-971-23	Sequence 23, Appl
	20	11.8	78.7	100	4	US-08-221-653-23	Sequence 23, Appl
	21	11.8	78.7	100	4	US-08-442-144A-23	Sequence 23, Appl
	22	11.8	78.7	100	4	US-08-441-970-23	Sequence 23, Appl
	23	11.4	76.0	15	4	US-09-081-646-198	Sequence 198, App
	24	11.4	76.0	20	3	US-09-280-799-190	Sequence 190, App
	25	11.4	76.0	26	2	US-08-759-581B-16	Sequence 16, Appl
	26	11.4	76.0	26	4	US-09-304-711-16	Sequence 16, Appl
c	27	11	73.3	14	5	PCT-US96-05611A-16	Sequence 16, Appl
c	28	11	73.3	15	4	US-08-268-381-1	Sequence 1, Appli
c	29	11	73.3	20	3	US-09-286-904-77	Sequence 77, Appl
c	30	11	73.3	27	1	US-08-083-948-9	Sequence 9, Appli
c	31	11	73.3	27	1	US-08-393-785-9	Sequence 9, Appli
c	32	11	73.3	27	1	US-08-475-694-9	Sequence 9, Appli
c	33	11	73.3	27	1	US-08-712-057-9	Sequence 9, Appli
	34	11	73.3	28	3	US-08-441-971-73	Sequence 73, Appl
	35	11	73.3	28	4	US-08-221-653-73	Sequence 73, Appl
	36	11	73.3	28	4	US-08-442-144A-73	Sequence 73, Appl
	37	11	73.3	28	4	US-08-441-970-73	Sequence 73, Appl
	38	11	73.3	30	4	US-09-243-374-9	Sequence 9, Appli
	39	11	73.3	30	6	5310667-15	Patent No. 5310667
c	40	11	73.3	33	1	US-08-438-639-21	Sequence 21, Appl
c	41	11	73.3	33	1	US-07-813-338A-21	Sequence 21, Appl
c	42	11	73.3	33	3	US-08-441-971-96	Sequence 96, Appl
c	43	11	73.3	33	4	US-08-221-653-96	Sequence 96, Appl
c	44	11	73.3	33	4	US-08-442-144A-96	Sequence 96, Appl
c	45	11	73.3	33	4	US-08-441-970-96	Sequence 96, Appl

ALIGNMENTS

```
RESULT   1
US-08-991-830A-3
; Sequence 3, Application US/08991830A
; Patent No. 6027892
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Esther H.
;    APPLICANT:  Pirollo, Kathleen F.
;    TITLE OF INVENTION:  Compositions and Methods for Reducing Radiation and Drug R
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sana A. Pratt
;      STREET:  10821 Hillbrooke Lane
;      CITY:  Potomac
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  20854
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.5
;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/991,830A
;      FILING DATE:  16 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/034,160
;      FILING DATE:  30 December 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sana A. Pratt
;      REGISTRATION NUMBER:  39,441
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 294-9171
;      TELEFAX:  (301) 294-7357
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  DNA
US-08-991-830A-3


  Query Match             100.0%;  Score 15;  DB 3;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
```

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          ||||||||||||||||
Db      1 TCCATGGTGCTCACT 15


RESULT   2
US-08-435-350-4/c
; Sequence 4, Application US/08435350
; Patent No. 5599704
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  TREATMENT OF BREAST CANCER
;    NUMBER OF SEQUENCES:  118
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,350
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936,531
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/245
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-435-350-4


  Query Match             100.0%;  Score 15;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||||||||||||
Db     21 TCCATGGTGCTCACT 7


RESULT   3
US-08-740-821-1
; Sequence 1, Application US/08740821
; Patent No. 5910583
;  GENERAL INFORMATION:
;    APPLICANT:  Marks, Jeffrey R.
;    APPLICANT:  Vaughn, James P.
;    APPLICANT:  Iglehart, James D.
;    TITLE OF INVENTION:  ANTISENSE OLIGONUCLEOTIDES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Bell, Seltzer, Park & Gibson, P.A.
;      STREET:  Post Office Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5910583th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/740,821
;      FILING DATE:  04-NOV-1996
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5405-134
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "OLIGONUCLEOTIDE"
US-08-740-821-1


  Query Match             93.3%;  Score 14;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 47;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcac 14
          ||||||||||||||
Db      2 TCCATGGTGCTCAC 15


RESULT   4
US-09-089-111-3
; Sequence 3, Application US/09089111
; Patent No. 6162965
;  GENERAL INFORMATION:
;    APPLICANT:  Hansen, Genevieve
;    TITLE OF INVENTION:  Plant Transformation Methods
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  No. 6162965artis Corporation
;      STREET:  3054 Cornwallis Rd.
;      CITY:  Research Triangle Park
;      STATE:  NC
;      COUNTRY:  USA
;      ZIP:  27709
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/089,111
;      FILING DATE:  02-Jun-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hoxie, Thomas
;      REGISTRATION NUMBER:  32,993
;      REFERENCE/DOCKET NUMBER:  CGC1928/R
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-541-8614
;      TELEFAX:  919-541-8689
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
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```
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     IMMEDIATE SOURCE:
;       CLONE:  MTL (P)
US-09-089-111-3


  Query Match             86.7%;  Score 13;  DB 4;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctca 13
          |||||||||||||
Db      6 TCCATGGTGCTCA 18


RESULT   5
US-08-463-691-18
; Sequence 18, Application US/08463691
; Patent No. 6165712
;  GENERAL INFORMATION:
;    APPLICANT:  J. Gordon Foulkes et al.
;    TITLE OF INVENTION:  Methods of Transcriptionally
;    TITLE OF INVENTION:  Modulating Expression of Viral Genes and Genes Useful for the
;    TITLE OF INVENTION:  Production of Proteins
;    NUMBER OF SEQUENCES:  20
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  John P. White, Esq.
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,691
;      FILING DATE:  5-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  26134-G1Z
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-591-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-463-691-18


  Query Match             86.7%;  Score 13;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 catggtgctcact 15
          |||||||||||||
Db      1 CATGGTGCTCACT 13


RESULT   6
US-08-255-236-6
; Sequence 6, Application US/08255236
; Patent No. 6203976
; GENERAL INFORMATION:
;  APPLICANT:  Foulkes, J. Gordon
;  TITLE OF INVENTION:  METHODS OF TRANSCRIPTIONALLY MODULATING EXPRESSION OF
;  TITLE OF INVENTION:  VIRAL GENES AND GENES USEFUL FOR PRODUCTION OF PROTEINS
;  FILE REFERENCE:  26134g1
;  CURRENT APPLICATION NUMBER: US/08/255,236
;  CURRENT FILING DATE:  1994-06-07
;  NUMBER OF SEQ ID NOS:  18
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 26
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-08-255-236-6


  Query Match             86.7%;  Score 13;  DB 4;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 catggtgctcact 15
          |||||||||||||
Db      1 catggtgctcact 13


RESULT   7
US-08-229-528-5/c
; Sequence 5, Application US/08229528
; Patent No. 5837447
;  GENERAL INFORMATION:
;    APPLICANT:  GORSKI, Jack
;    TITLE OF INVENTION:  MONITORING AN IMMUNE RESPONSE BY ANALYSIS OF AMPLIFIED IM
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  P. O. Box 1497
;      CITY:  Madison
;      STATE:  Wisconsin
;      COUNTRY:  USA
;      ZIP:  53701-1497
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette,3.50 inch, 1.44 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  MS-DOS 3.3
;      SOFTWARE:  WordPerfect, Version 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,528
;      FILING DATE:  18-APR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/868,569
;      FILING DATE:  15-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Scanlon, William J.
;      REGISTRATION NUMBER:  30,136
;      REFERENCE/DOCKET NUMBER:  30383/133
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 258-4284
;      TELEFAX:  (608) 258-4258
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
US-08-229-528-5
```

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  Query Match             82.7%;  Score 12.4;  DB 2;  Length 22;
  Best Local Similarity   92.9%;  Pred. No. 3.4e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcac 14
          |||| |||||||||
Db     21 TCCAAGGTGCTCAC 8


RESULT   8
US-09-338-907-248
; Sequence 248, Application US/09338907
; Patent No. 6265546
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Ilya, Chumakov
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: PROSTATE CANCER GENE
;  FILE REFERENCE: GENSET.18CP1CP
;  CURRENT APPLICATION NUMBER: US/09/338,907
;  CURRENT FILING DATE: 1999-06-23
;  EARLIER APPLICATION NUMBER: 08/996,306
;  EARLIER FILING DATE: 1997-12-22
;  EARLIER APPLICATION NUMBER: 60/099,658
;  EARLIER FILING DATE: 1998-09-09
;  EARLIER APPLICATION NUMBER: 09/218,207
;  EARLIER FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 248
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 99-148-366
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: polymorphic base G
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 99-148-366.mis1
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 99-148-366.mis2
US-09-338-907-248


  Query Match             82.7%;  Score 12.4;  DB 4;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 3.5e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcac 14
          ||| ||||||||||
Db     18 tccctggtgctcac 31


RESULT   9
US-09-218-207-248
; Sequence 248, Application US/09218207
; Patent No. 6346381
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Ilya, Chumakov
;  APPLICANT: Bougueleret, Lydie
;  TITLE OF INVENTION: Prostate cancer gene
;  FILE REFERENCE: GENSET.018CP1
;  CURRENT APPLICATION NUMBER: US/09/218,207
;  CURRENT FILING DATE: 1998-12-22
;  EARLIER APPLICATION NUMBER: 08/996,306
;  EARLIER FILING DATE: 1997-12-22
;  EARLIER APPLICATION NUMBER: 60/099,658
;  EARLIER FILING DATE: 1998-09-09
;  NUMBER OF SEQ ID NOS: 578
;  SOFTWARE: Patent.pm
; SEQ ID NO 248
;   LENGTH: 47
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 1..47
;   OTHER INFORMATION: polymorphic fragment 99-148-366
;   FEATURE:
;   NAME/KEY: allele
;   LOCATION: 24
;   OTHER INFORMATION: polymorphic base G
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..23
;   OTHER INFORMATION: potential microsequencing oligo 99-148-366.mis1
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 25..47
;   OTHER INFORMATION: complement potential microsequencing oligo 99-148-366.mis2
US-09-218-207-248


  Query Match             82.7%;  Score 12.4;  DB 4;  Length 47;
  Best Local Similarity   92.9%;  Pred. No. 3.5e+02;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcac 14
          ||| ||||||||||
Db     18 tccctggtgctcac 31


RESULT  10
US-08-503-730-44/c
; Sequence 44, Application US/08503730
; Patent No. 5780269
;  GENERAL INFORMATION:
;    APPLICANT:  Inouye, Sumiko
;    APPLICANT:  Inouye, Masayori
;    TITLE OF INVENTION:  NEW HYBRID MOLECULES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,730
;      FILING DATE:  18-JUL-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/817,430
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  377(913).6277P
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  27 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-503-730-44


  Query Match             80.0%;  Score 12;  DB 1;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctca 13
          ||||||||||||
Db     16 CCATGGTGCTCA 5


RESULT  11
US-08-503-730-29/c
; Sequence 29, Application US/08503730
; Patent No. 5780269
;  GENERAL INFORMATION:
;    APPLICANT:  Inouye, Sumiko
;    APPLICANT:  Inouye, Masayori
;    TITLE OF INVENTION:  NEW HYBRID MOLECULES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,730
;      FILING DATE:  18-JUL-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/817,430
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  377(913).6277P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  53 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  both
US-08-503-730-29


  Query Match             80.0%;  Score 12;  DB 1;  Length 53;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctca 13
          ||||||||||||
Db     13 CCATGGTGCTCA 2
```

```
RESULT  12
US-08-503-730-30/c
; Sequence 30, Application US/08503730
; Patent No. 5780269
;  GENERAL INFORMATION:
;    APPLICANT:  Inouye, Sumiko
;    APPLICANT:  Inouye, Masayori
;    TITLE OF INVENTION:  NEW HYBRID MOLECULES
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Weiser & Associates
;      STREET:  230 South Fifteenth Street Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/503,730
;      FILING DATE:  18-JUL-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/817,430
;      FILING DATE:  06-JAN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  377(913).6277P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  62 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  both
US-08-503-730-30


  Query Match             80.0%;  Score 12;  DB 1;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 5.8e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctca 13
          ||||||||||||
Db     13 CCATGGTGCTCA 2


RESULT  13
US-08-832-468-6
; Sequence 6, Application US/08832468
; Patent No. 5962237
;  GENERAL INFORMATION:
;    APPLICANT:  Ts'o, Paul O.P.
;    APPLICANT:  Wang, Zheng-Pin
;    APPLICANT:  Lesko, Stephen A.
;    APPLICANT:  Nelson, William G.
;    APPLICANT:  Partin, Alan W.
;    TITLE OF INVENTION:  A METHOD OF ENRICHING RARE CELLS
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Leydig, Voit & Mayer, Ltd.
;      STREET:  700 Thirteenth St., NW
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  US
;      ZIP:  20005
;    COMPUTER READABLE FORM:
```

```
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/832,468
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60-014929
;      FILING DATE:  05-APR-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jay, Jeremy M.
;      REGISTRATION NUMBER:  33587
;      REFERENCE/DOCKET NUMBER:  72466
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-737-6770
;      TELEFAX:  202-737-6776
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  50 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid (synthetic DNA)
US-08-832-468-6


  Query Match             78.7%;  Score 11.8;  DB 2;  Length 50;
  Best Local Similarity   86.7%;  Pred. No. 7.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||| |||||| ||
Db     19 TCCATAGTGCTCCCT 33


RESULT  14
US-08-363-240A-1077/c
; Sequence 1077, Application US/08363240A
; Patent No. 5705388
;  GENERAL INFORMATION:
;    APPLICANT:  Couture, Larry
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Bisgaier, Charles
;    APPLICANT:  Pape, Michael
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  PREVENTION, INHIBITION OF
;    TITLE OF INVENTION:  PROGRESSION AND REGRESSION
;    TITLE OF INVENTION:  OF VASCULAR DISEASES
;    NUMBER OF SEQUENCES:  1243
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/363,240A
;      FILING DATE:  December 23, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  210/096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1077:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  54 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-363-240A-1077


  Query Match             78.7%;  Score 11.8;  DB 1;  Length 54;
  Best Local Similarity   86.7%;  Pred. No. 7.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db     26 TCTCTGGTGCTCACT 12


RESULT  15
US-08-584-040-4423/c
; Sequence 4423, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4423:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  54 base pairs
;      TYPE:  nucleic acid
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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-584-040-4423


  Query Match             78.7%;  Score 11.8;  DB 4;  Length 54;
  Best Local Similarity   86.7%;  Pred. No. 7.4e+02;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
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Search completed: July 21, 2002, 03:52:46
Job time: 17781 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 02:55:01 ; Search time 2682.64 Seconds
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Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 11371150

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	100.0	15	18	US-09-406-643-255	Sequence 255, App
	2	15	100.0	15	18	US-09-480-143-3	Sequence 3, Appli
	3	15	100.0	15	28	US-09-716-320-3	Sequence 3, Appli
	4	15	100.0	19	26	US-09-669-187A-13	Sequence 13, Appl
	5	15	100.0	19	33	US-09-888-326-66	Sequence 66, Appl
	6	15	100.0	19	37	US-10-017-995-13	Sequence 13, Appl
c	7	15	100.0	24	3	US-07-936-531A-4	Sequence 4, Appli
c	8	15	100.0	24	11	US-08-780-074-4	Sequence 4, Appli
	9	15	100.0	51	56	US-60-172-373-13441	Sequence 13441, A
c	10	14	93.3	17	18	US-09-474-432B-576	Sequence 576, App
c	11	14	93.3	17	18	US-09-476-387-575	Sequence 575, App
c	12	14	93.3	17	31	US-09-825-805-575	Sequence 575, App
	13	14	93.3	51	29	US-09-726-173A-2507	Sequence 2507, Ap
c	14	14	93.3	51	56	US-60-172-360-22019	Sequence 22019, A
c	15	14	93.3	51	66	US-60-278-232-5518	Sequence 5518, Ap
c	16	13.4	89.3	24	15	US-09-147-773A-1	Sequence 1, Appli
c	17	13.4	89.3	25	35	US-09-956-584-426077	Sequence 426077,
c	18	13.4	89.3	25	62	US-60-234-017-451230	Sequence 451230,
	19	13.4	89.3	73	21	US-09-540-766-63011	Sequence 63011, A
	20	13	86.7	14	10	US-08-666-341A-105	Sequence 105, App
	21	13	86.7	14	17	US-09-341-700A-1137	Sequence 1137, Ap
c	22	13	86.7	15	18	US-09-406-643-256	Sequence 256, App
	23	13	86.7	16	17	US-09-341-700A-325	Sequence 325, App
c	24	13	86.7	19	1	PCT-US01-25502-3	Sequence 3, Appli
c	25	13	86.7	19	16	US-09-234-208B-3	Sequence 3, Appli
c	26	13	86.7	19	24	US-09-630-155-3	Sequence 3, Appli
	27	13	86.7	20	18	US-09-490-094-3	Sequence 3, Appli
c	28	13	86.7	20	28	US-09-715-418-9	Sequence 9, Appli
	29	13	86.7	20	29	US-09-741-297-3	Sequence 3, Appli
	30	13	86.7	26	3	US-07-644-233-18	Sequence 18, Appl
	31	13	86.7	26	5	US-08-137-689-18	Sequence 18, Appl

	32	13	86.7	26	5	US-08-139-639-18	Sequence 18, Appl
c	33	13	86.7	39	68	US-60-298-340-23	Sequence 23, Appl
	34	12.4	82.7	20	1	PCT-US00-00325-94	Sequence 94, Appl
	35	12.4	82.7	20	16	US-09-232-785-94	Sequence 94, Appl
	36	12.4	82.7	20	16	US-09-232-884-94	Sequence 94, Appl
c	37	12.4	82.7	22	3	US-07-868-569-5	Sequence 5, Appli
c	38	12.4	82.7	25	17	US-09-396-196F-53471	Sequence 53471, A
c	39	12.4	82.7	25	17	US-09-396-196F-53472	Sequence 53472, A
c	40	12.4	82.7	25	26	US-09-660-220-50129	Sequence 50129, A
c	41	12.4	82.7	25	26	US-09-660-220-137820	Sequence 137820,
c	42	12.4	82.7	25	35	US-09-954-427-52165	Sequence 52165, A
c	43	12.4	82.7	25	62	US-60-233-166-52165	Sequence 52165, A
	44	12.4	82.7	25	74	US-60-353-987-688919	Sequence 688919,
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ALIGNMENTS

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; Sequence 255, Application US/09406643
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Ludwig, Janos
;  APPLICANT:  Sproat, Brian
;  APPLICANT:  Beigelman, Leonid
;  TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
;  FILE REFERENCE: MBHB00-874-A (237/197)
;  CURRENT APPLICATION NUMBER: US/09/406,643
;  CURRENT FILING DATE:  1999-09-27
;  PRIOR APPLICATION NUMBER: US 08/879,078
;  PRIOR FILING DATE: 1997-06-19
;  PRIOR APPLICATION NUMBER: US 08/878,640
;  PRIOR FILING DATE: 1997-06-19
;  NUMBER OF SEQ ID NOS: 2606
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 255
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-406-643-255


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Db     15 TCCATGGTGCTCACT 1


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US-09-480-143-3
; Sequence 3, Application US/09480143
;  GENERAL INFORMATION:
;    APPLICANT:  Chang, Esther H.
;    APPLICANT:  Pirollo, Kathleen F.
;    TITLE OF INVENTION:  Compositions and Methods for Reducing Radiation and Drug Resis
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sana A. Pratt
;      STREET:  10821 Hillbrooke Lane
;      CITY:  Potomac
;      STATE:  MARYLAND
;      COUNTRY:  USA
;      ZIP:  20854
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Apple Macintosh
;      OPERATING SYSTEM:  Macintosh 7.5
;      SOFTWARE:  Microsoft Word 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/480,143
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/991,830
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sana A. Pratt
;      REGISTRATION NUMBER:  39,441
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (301) 294-9171
;      TELEFAX:  (301) 294-7357
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  Nucleic acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  DNA
US-09-480-143-3


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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      1 TCCATGGTGCTCACT 15


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; Sequence 3, Application US/09716320
; GENERAL INFORMATION:
;  APPLICANT: Chang, Esther H
;  APPLICANT:  Pirollo, Kathleen F
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING RADIATION AND DRUG RESIS
;  FILE REFERENCE: 2444-109
;  CURRENT APPLICATION NUMBER: US/09/716,320
;  CURRENT FILING DATE:  2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/480,143
;  PRIOR FILING DATE: 2000-01-10
;  PRIOR APPLICATION NUMBER: US 08/991,830
;  PRIOR FILING DATE: 1997-12-16
;  PRIOR APPLICATION NUMBER: US 60/034,160
;  PRIOR FILING DATE: 1996-12-30
;  PRIOR APPLICATION NUMBER: US 09/601,444
;  PRIOR FILING DATE: 2001-01-04
;  PRIOR APPLICATION NUMBER: PCT/US98/24657
;  PRIOR FILING DATE: 1998-11-19
;  PRIOR APPLICATION NUMBER: US 60/066,188
;  PRIOR FILING DATE: 1997-11-19
;  PRIOR APPLICATION NUMBER: US 60/083,175
;  PRIOR FILING DATE: 1998-04-27
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Human
US-09-716-320-3


  Query Match            100.0%;  Score 15;  DB 28;  Length 15;
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Db      1 tccatggtgctcact 15
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; Sequence 13, Application US/09669187A
; GENERAL INFORMATION:
;  APPLICANT:  Krieg, Arthur M.
;  APPLICANT:  Schetter, Christian
;  APPLICANT:  Vollmer, Jorg
;  TITLE OF INVENTION:  Immunostimulatory Nucleic Acids
;  FILE REFERENCE:  C1039/7035 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/09/669,187A
;  CURRENT FILING DATE:  2000-09-25
;  PRIOR APPLICATION NUMBER:  US 60/156,113
;  PRIOR FILING DATE:  1999-09-25
;  PRIOR APPLICATION NUMBER:  US 60/156,135
;  PRIOR FILING DATE:  1999-09-27
;  PRIOR APPLICATION NUMBER:  US 60/227,436
;  PRIOR FILING DATE:  2000-08-23
;  NUMBER OF SEQ ID NOS:  1145
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-09-669-187A-13


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Db      4 tccatggtgctcact 18


RESULT   5
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; Sequence 66, Application US/09888326
; GENERAL INFORMATION:
;  APPLICANT: Weiner, George
;  APPLICANT:  Hartmann, Gunther
;  TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
;  TITLE OF INVENTION:  Cell Lysis and Treating Cancer
;  FILE REFERENCE: C1039/7052 (AWS)
;  CURRENT APPLICATION NUMBER: US/09/888,326
;  CURRENT FILING DATE:  2001-06-22
;  PRIOR APPLICATION NUMBER: US 60/213,346
;  PRIOR FILING DATE: 2000-06-22
;  NUMBER OF SEQ ID NOS: 848
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: phosphorothioate backbone
US-09-888-326-66


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Qy      1 tccatggtgctcact 15
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Db      4 tccatggtgctcact 18


RESULT   6
US-10-017-995-13
; Sequence 13, Application US/10017995
; GENERAL INFORMATION:
;  APPLICANT: Bratzler, Robert L.
;  TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
;  FILE REFERENCE: C1037/7025 (HCL/MAT)
;  CURRENT APPLICATION NUMBER: US/10/017,995
;  CURRENT FILING DATE:  2001-12-18
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;  PRIOR FILING DATE: 2000-12-14
;  NUMBER OF SEQ ID NOS: 1093
;  SOFTWARE: FastSEQ for Windows Version 3.0
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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Sequence
US-10-017-995-13


  Query Match             100.0%;  Score 15;  DB 37;  Length 19;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
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Db      4 tccatggtgctcact 18


RESULT   7
US-07-936-531A-4/c
; Sequence 4, Application US/07936531A
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  TREATMENT OF BREAST CANCER
;    NUMBER OF SEQUENCES:  118
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/936,531A
;      FILING DATE:  19920826
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    none
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/245
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  24
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-936-531A-4


  Query Match             100.0%;  Score 15;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||||||||||||
Db     21 TCCATGGTGCTCACT 7


RESULT   8
US-08-780-074-4/c
; Sequence 4, Application US/08780074
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  TREATMENT OF BREAST CANCER
;    NUMBER OF SEQUENCES:  118
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/780,074
;      FILING DATE:  23-DEC-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/936,531
;      FILING DATE:  August 26, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/245
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-780-074-4


  Query Match             100.0%;  Score 15;  DB 11;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 6.8e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||||||||||||
Db     21 TCCATGGTGCTCACT 7


RESULT   9
US-60-172-373-13441
; Sequence 13441, Application US/60172373
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polym
;  FILE REFERENCE: GX-0006 P
;  CURRENT APPLICATION NUMBER: US/60/172,373
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 25,772
;  SOFTWARE: PERL Program
; SEQ ID NO 13441
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: SNP00025363
;   FEATURE:
;   NAME/KEY: snp
;   LOCATION: 26
;   OTHER INFORMATION: 200140.2, 2095, G->A
US-60-172-373-13441


  Query Match             100.0%;  Score 15;  DB 56;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 7.4e+02;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||||||||||||
Db     36 tccatggtgctcact 50


RESULT  10
US-09-474-432B-576/c
; Sequence 576, Application US/09474432B
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Burgin, Alex
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka
;  APPLICANT:  Sweedler, David
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucl
;  FILE REFERENCE: MBHB00-831-B (247/276)
;  CURRENT APPLICATION NUMBER: US/09/474,432B
;  CURRENT FILING DATE:  1999-12-19
;  PRIOR APPLICATION NUMBER: US 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  PRIOR APPLICATION NUMBER: US 60/084,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: US 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: US 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 1526
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 576
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-474-432B-576


  Query Match             93.3%;  Score 14;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctcact 15
          ||||||||||||||
```

```
Db      17 CCATGGTGCTCACT 4


RESULT  11
US-09-476-387-575/c
; Sequence 575, Application US/09476387
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
;  FILE REFERENCE: MBHB00-831-C (249/073)
;  CURRENT APPLICATION NUMBER: US/09/476,387
;  CURRENT FILING DATE:  2001-04-04
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1524
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 575
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-476-387-575


  Query Match             93.3%;  Score 14;  DB 18;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctcact 15
          ||||||||||||||
Db     17 CCATGGTGCTCACT 4


RESULT  12
US-09-825-805-575/c
; Sequence 575, Application US/09825805
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Beigelman, Leo
;  APPLICANT:  Beaudry, Amber
;  APPLICANT:  Karpeisky, Alex
;  APPLICANT:  Adamic, Jasenka Matulic
;  APPLICANT:  Sweedler, Dave
;  APPLICANT:  Zinnen, Shawn
;  TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
;  FILE REFERENCE: MBHB00-831-F (400/009)
;  CURRENT APPLICATION NUMBER: US/09/825,805
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: 09/578,223
;  PRIOR FILING DATE: 2000-05-23
;  PRIOR APPLICATION NUMBER: 09/476,387
;  PRIOR FILING DATE: 1999-12-30
;  PRIOR APPLICATION NUMBER: 09/474,432
;  PRIOR FILING DATE: 1999-12-29
;  PRIOR APPLICATION NUMBER: 09/301,511
;  PRIOR FILING DATE: 1999-04-28
;  PRIOR APPLICATION NUMBER: 09/186,675
;  PRIOR FILING DATE: 1998-11-04
;  PRIOR APPLICATION NUMBER: 60/083,727
;  PRIOR FILING DATE: 1998-04-29
;  PRIOR APPLICATION NUMBER: 60/064,866
;  PRIOR FILING DATE: 1997-11-05
;  NUMBER OF SEQ ID NOS: 1558
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 575
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-825-805-575


  Query Match             93.3%;  Score 14;  DB 31;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctcact 15
          ||||||||||||||
Db     17 CCATGGTGCTCACT 4


RESULT  13
US-09-726-173A-2507
; Sequence 2507, Application US/09726173A
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  Leach, Martin D.
;  TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AN
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: 15966-600
;  CURRENT APPLICATION NUMBER: US/09/726,173A
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: 60/168,138
;  PRIOR FILING DATE: 1999-11-30
;  NUMBER OF SEQ ID NOS: 7024
;  SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 2507
;   LENGTH: 51
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (26)...(0)
;   OTHER INFORMATION: 1 of 2 allelic variants (2508 is other entry)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Accession number cg39714236
US-09-726-173A-2507


  Query Match             93.3%;  Score 14;  DB 29;  Length 51;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctcact 15
          ||||||||||||||
Db     17 ccatggtgctcact 30


RESULT  14
US-60-172-360-22019/c
; Sequence 22019, Application US/60172360
; GENERAL INFORMATION:
;  APPLICANT: Morris, MacDonald
;  APPLICANT: Lal, Preeti
;  APPLICANT: Diep, Dinh
;  TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
;  TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
;  FILE REFERENCE: GX-0007 P
;  CURRENT APPLICATION NUMBER: US/60/172,360
;  CURRENT FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 29838
;  SOFTWARE: PERL Program
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; SEQ ID NO 22019
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00037393
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 383094.3, 615, C->T
US-60-172-360-22019

Query Match 93.3%; Score 14; DB 56; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 tccatggtgctcac 14
           ||||||||||||||
Db      29 TCCATGGTGCTCAC 16
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RESULT 15
US-60-278-232-5518/c
; Sequence 5518, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; TITLE OF INVENTION: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557
; SOFTWARE: PERL Program
; SEQ ID NO 5518
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: SNP00047234
; FEATURE:
; NAME/KEY: snp
; LOCATION: 26
; OTHER INFORMATION: 245722.5, 91, G->A
US-60-278-232-5518

Query Match 93.3%; Score 14; DB 66; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       2 ccatggtgctcact 15
           ||||||||||||||
Db      35 CCATGGTGCTCACT 22
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Search completed: July 21, 2002, 04:41:36
Job time: 6395 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 03:21:26 ; Search time 195.72 Seconds
(without alignments)
144.300 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1225709 seqs, 941415038 residues

Total number of hits satisfying chosen parameters: 629858

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15	100.0	15	5	US-09-498-824A-255	Sequence 255, App
c	2	15	100.0	17	6	US-10-163-552-38	Sequence 38, Appl
	3	15	100.0	19	6	US-10-112-653-13	Sequence 13, Appl
c	4	14	93.3	17	6	US-10-163-552-37	Sequence 37, Appl
c	5	13	86.7	15	5	US-09-498-824A-256	Sequence 256, App
c	6	13	86.7	17	6	US-10-163-552-39	Sequence 39, Appl
c	7	13	86.7	19	5	US-09-638-834A-3	Sequence 3, Appli
c	8	13	86.7	39	6	US-10-173-461-24	Sequence 24, Appl
	9	12.4	82.7	71	5	US-09-539-331D-9880	Sequence 9880, Ap
c	10	12	80.0	15	5	US-09-498-824A-1	Sequence 1, Appli
c	11	11.8	78.7	17	6	US-10-138-674-6193	Sequence 6193, Ap
c	12	11.8	78.7	17	6	US-10-138-674-6194	Sequence 6194, Ap
c	13	11.8	78.7	17	6	US-10-138-674-8504	Sequence 8504, Ap
c	14	11.8	78.7	19	5	US-09-909-567B-34	Sequence 34, Appl
c	15	11.8	78.7	54	6	US-10-138-674-11609	Sequence 11609, A
c	16	11.8	78.7	60	6	US-10-149-187-4	Sequence 4, Appli
	17	11.8	78.7	100	6	US-10-104-545-3	Sequence 3, Appli
	18	11.4	76.0	20	5	US-09-922-549B-20	Sequence 20, Appl
	19	11.4	76.0	20	5	US-09-937-473C-190	Sequence 190, App
	20	11.4	76.0	24	5	US-09-792-468-2	Sequence 2, Appli
	21	11.4	76.0	26	6	US-10-027-632-52388	Sequence 52388, A
	22	11.4	76.0	66	5	US-09-284-349A-2	Sequence 2, Appli
c	23	11	73.3	14	4	US-08-431-644B-16	Sequence 16, Appl
c	24	11	73.3	99	5	US-09-975-254-16421	Sequence 16421, A
c	25	10.8	72.0	18	6	US-10-108-732-12	Sequence 12, Appl
	26	10.8	72.0	20	5	US-09-544-398A-404	Sequence 404, App
	27	10.8	72.0	20	5	US-09-544-398B-404	Sequence 404, App
c	28	10.8	72.0	24	5	US-09-978-403A-53	Sequence 53, Appl
c	29	10.8	72.0	24	5	US-09-978-544A-53	Sequence 53, Appl
c	30	10.8	72.0	24	5	US-09-978-681A-53	Sequence 53, Appl
c	31	10.8	72.0	24	5	US-09-978-757A-53	Sequence 53, Appl
c	32	10.8	72.0	24	5	US-09-978-564A-53	Sequence 53, Appl
c	33	10.8	72.0	24	5	US-09-999-831A-53	Sequence 53, Appl
c	34	10.8	72.0	24	5	US-09-999-829A-53	Sequence 53, Appl
c	35	10.8	72.0	24	5	US-09-978-375A-53	Sequence 53, Appl
c	36	10.8	72.0	24	5	US-09-978-423A-53	Sequence 53, Appl
c	37	10.8	72.0	24	6	US-10-013-921A-53	Sequence 53, Appl
c	38	10.8	72.0	24	6	US-10-013-929A-53	Sequence 53, Appl
c	39	10.8	72.0	24	6	US-10-013-918A-53	Sequence 53, Appl
c	40	10.8	72.0	24	6	US-10-017-082A-53	Sequence 53, Appl
c	41	10.8	72.0	24	6	US-10-017-085A-53	Sequence 53, Appl
c	42	10.8	72.0	24	6	US-10-013-916A-53	Sequence 53, Appl
c	43	10.8	72.0	24	6	US-10-017-086A-53	Sequence 53, Appl
c	44	10.8	72.0	24	6	US-10-013-925A-53	Sequence 53, Appl
c	45	10.8	72.0	24	6	US-10-017-081A-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-498-824A-255/c
; Sequence 255, Application US/09498824A
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Ludwig, Janos
; APPLICANT: Sproat, Brian
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
; FILE REFERENCE: MBHB00-874-D (247/280)
; CURRENT APPLICATION NUMBER: US/09/498,824A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 09/406,643
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 08/878,640
; PRIOR FILING DATE: 1997-06-19
; PRIOR APPLICATION NUMBER: US 08/879,078
; PRIOR FILING DATE: 1997-06-19
; NUMBER OF SEQ ID NOS: 3516
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 255
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-498-824A-255

Query Match 100.0%; Score 15; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tccatggtgctcact 15
||||||||||||||||
Db 15 TCCATGGTGCTCACT 1

RESULT 2
US-10-163-552-38/c
; Sequence 38, Application US/10163552
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to l
; TITLE OF INVENTION: HER2
; FILE REFERENCE: MBHB01-1653-A (400/014)
; CURRENT APPLICATION NUMBER: US/10/163,552
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 1997
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 38
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-163-552-38


  Query Match             100.0%;  Score 15;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          |||||||||||||||
Db     16 TCCATGGTGCTCACT 2


RESULT   3
US-10-112-653-13
; Sequence 13, Application US/10112653
; GENERAL INFORMATION:
;  APPLICANT: Krieg, Arthur M.
;  APPLICANT:  Berg, Daniel J.
;  TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
;  TITLE OF INVENTION:  TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
;  FILE REFERENCE: C01039/70060(AWS)
;  CURRENT APPLICATION NUMBER: US/10/112,653
;  CURRENT FILING DATE:  2002-03-29
;  PRIOR APPLICATION NUMBER: US 60/279,642
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 1040
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-13


  Query Match             100.0%;  Score 15;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          |||||||||||||||
Db      4 tccatggtgctcact 18


RESULT   4
US-10-163-552-37/c
; Sequence 37, Application US/10163552
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
;  TITLE OF INVENTION:  HER2
;  FILE REFERENCE: MBHB01-1653-A (400/014)
;  CURRENT APPLICATION NUMBER: US/10/163,552
;  CURRENT FILING DATE:  2002-06-06
;  NUMBER OF SEQ ID NOS: 1997
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 37
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-163-552-37


  Query Match             93.3%;  Score 14;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctcact 15
          ||||||||||||||
Db     17 CCATGGTGCTCACT 4


RESULT   5
US-09-498-824A-256/c
; Sequence 256, Application US/09498824A
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Ludwig, Janos
;  APPLICANT:  Sproat, Brian
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
;  FILE REFERENCE: MBHB00-874-D (247/280)
;  CURRENT APPLICATION NUMBER: US/09/498,824A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: US 09/406,643
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 08/878,640
;  PRIOR FILING DATE: 1997-06-19
;  PRIOR APPLICATION NUMBER: US 08/879,078
;  PRIOR FILING DATE: 1997-06-19
;  NUMBER OF SEQ ID NOS: 3516
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 256
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-498-824A-256


  Query Match             86.7%;  Score 13;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 9.1e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctca 13
          |||||||||||||
Db     13 TCCATGGTGCTCA 1


RESULT   6
US-10-163-552-39/c
; Sequence 39, Application US/10163552
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to le
;  TITLE OF INVENTION:  HER2
;  FILE REFERENCE: MBHB01-1653-A (400/014)
;  CURRENT APPLICATION NUMBER: US/10/163,552
;  CURRENT FILING DATE:  2002-06-06
;  NUMBER OF SEQ ID NOS: 1997
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-163-552-39


  Query Match             86.7%;  Score 13;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctca 13
          |||||||||||||
Db     13 TCCATGGTGCTCA 1


RESULT   7
US-09-638-834A-3/c
; Sequence 3, Application US/09638834A
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; GENERAL INFORMATION:
;  APPLICANT: Clinton, Gail M.
;  TITLE OF INVENTION: Expression of Herstatin, an Alternative HER-2/NEU Product, in Cel
;  TITLE OF INVENTION:  Express either p185HER-2 or the EGF Receptor Inhibits Receptor A
;  TITLE OF INVENTION:  Growth
;  FILE REFERENCE: 49321-12
;  CURRENT APPLICATION NUMBER: US/09/638,834A
;  CURRENT FILING DATE:  2000-08-14
;  PRIOR APPLICATION NUMBER: US 09/234,208
;  PRIOR FILING DATE: 1999-01-20
;  PRIOR APPLICATION NUMBER: US 09/506,079
;  PRIOR FILING DATE: 2000-01-16
;  NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HER-2-specific oligonucleotide primer
US-09-638-834A-3


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  Best Local Similarity   100.0%;  Pred. No. 9.2e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctca 13
           |||||||||||||
Db      13 TCCATGGTGCTCA 1


RESULT   8
US-10-173-461-24/c
; Sequence 24, Application US/10173461
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN GROWTH FACTOR WITH HOMOLOGY
;  TITLE OF INVENTION:  EPIDERMAL GROWTH FACTOR, BGS-8, EXPRESSED HIGHLY IN IMMUNE TISSU
;  FILE REFERENCE: D0166 NP
;  CURRENT APPLICATION NUMBER: US/10/173,461
;  CURRENT FILING DATE:  2002-06-14
;  PRIOR APPLICATION NUMBER: US 60/298,340
;  PRIOR FILING DATE: 2001-06-14
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 39
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-173-461-24


  Query Match             86.7%;  Score 13;  DB 6;  Length 39;
  Best Local Similarity   100.0%;  Pred. No. 9.5e+02;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 catggtgctcact 15
           |||||||||||||
Db      39 CATGGTGCTCACT 27


RESULT   9
US-09-539-331D-9880
; Sequence 9880, Application US/09539331D
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.
;  APPLICANT:  Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.
;  APPLICANT:  Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.
;  APPLICANT:  Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CARDIOVASCULAR SYSTEM TISSUE
;  FILE REFERENCE: PD-1022 CIP
;  CURRENT APPLICATION NUMBER: US/09/539,331D
;  CURRENT FILING DATE:  2000-03-30
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 40961
;  SOFTWARE: PERL Program
; SEQ ID NO 9880
;   LENGTH: 71
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: hu00367562
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 17, 47
;   OTHER INFORMATION: a, t, c, g, or other
US-09-539-331D-9880


  Query Match             82.7%;  Score 12.4;  DB 5;  Length 71;
  Best Local Similarity   86.7%;  Pred. No. 2.1e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
           ||||||| ||| |||
Db      40 tccatggngctgact 54


RESULT  10
US-09-498-824A-1/c
; Sequence 1, Application US/09498824A
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Ludwig, Janos
;  APPLICANT:  Sproat, Brian
;  APPLICANT:  Beigelman, Leo
;  TITLE OF INVENTION: Compositions Having RNA Cleaving Activity
;  FILE REFERENCE: MBHB00-874-D (247/280)
;  CURRENT APPLICATION NUMBER: US/09/498,824A
;  CURRENT FILING DATE:  2000-02-04
;  PRIOR APPLICATION NUMBER: US 09/406,643
;  PRIOR FILING DATE: 1999-09-27
;  PRIOR APPLICATION NUMBER: US 08/878,640
;  PRIOR FILING DATE: 1997-06-19
;  PRIOR APPLICATION NUMBER: US 08/879,078
;  PRIOR FILING DATE: 1997-06-19
;  NUMBER OF SEQ ID NOS: 3516
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 15
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-498-824A-1


  Query Match             80.0%;  Score 12;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctc 12
           ||||||||||||
Db      12 TCCATGGTGCTC 1


RESULT  11
US-10-138-674-6193/c
; Sequence 6193, Application US/10138674
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
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;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6193
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-6193


  Query Match             78.7%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||  ||  |||||
Db     17 TCCATGTTGGTCACT 3


RESULT  12
US-10-138-674-6194/c
; Sequence 6194, Application US/10138674
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6194
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-6194


  Query Match             78.7%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||  ||  |||||
Db     16 TCCATGTTGGTCACT 2


RESULT  13
US-10-138-674-8504/c
; Sequence 8504, Application US/10138674
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8504
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-8504


  Query Match             78.7%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||  ||  |||||
Db     15 TCCATGTTGGTCACT 1


RESULT  14
US-09-909-567B-34/c
; Sequence 34, Application US/09909567B
; GENERAL INFORMATION:
;  APPLICANT: Macina, Roberto A.
;  APPLICANT:  Nair, Manoj
;  APPLICANT:  Chen, Seiyu
;  TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes
;  FILE REFERENCE: DEX-0214
;  CURRENT APPLICATION NUMBER: US/09/909,567B
;  CURRENT FILING DATE:  2001-07-20
;  PRIOR APPLICATION NUMBER: 60/219,834
;  PRIOR FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-909-567B-34


  Query Match             78.7%;  Score 11.8;  DB 5;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 4.4e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||  |||||||  ||
Db     16 TCCACGGTGCTCCCT 2


RESULT  15
US-10-138-674-11609/c
; Sequence 11609, Application US/10138674
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11609
;   LENGTH: 54
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Enzymatic Nucleic Acid
US-10-138-674-11609


  Query Match             78.7%;  Score 11.8;  DB 6;  Length 54;
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  Best Local Similarity   86.7%;  Pred. No. 4.5e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
           ||  ||||||||||
Db      26 TCTCTGGTGCTCACT 12


Search completed: July 21, 2002, 04:45:12
Job time: 5026 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 20, 2002, 22:39:45 ; Search time 1566.41 Seconds
(without alignments)
129.247 Million cell updates/sec

Title: US-09-716-320-3
Perfect score: 15
Sequence: 1 tccatggtgctcact 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 297742

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	13.4	89.3	75	10	BM023447	BM023447 ie80e10.y
	2	12.4	82.7	58	9	AI022662	AI022662 ox05h11.x
	3	12.4	82.7	74	9	AL362924	AL362924 AL362924
	4	12.4	82.7	77	10	W15664	W15664 mb52d02.r1
c	5	12.4	82.7	80	9	AV832470	AV832470 AV832470
c	6	12	80.0	62	12	AZ648327	AZ648327 1M0517K13
	7	12	80.0	82	12	TA138D06P	AL465857 T. brucei
c	8	12	80.0	85	9	AI930840	AI930840 sb43a06.y
	9	12	80.0	90	9	AA690354	AA690354 vt31b01.r
c	10	12	80.0	92	12	AZ590927	AZ590927 1M0400G16
c	11	11.8	78.7	38	12	TA358F01P	AL494114 T. brucei
	12	11.8	78.7	65	9	AA285022	AA285022 zt25e10.s
	13	11.8	78.7	72	12	AZ799758	AZ799758 2M0057G19
c	14	11.8	78.7	89	10	BI472373	BI472373 fs02d01.y
	15	11.8	78.7	91	9	AV834264	AV834264 AV834264
	16	11.8	78.7	92	10	D18160	D18160 MUSGS00418
	17	11.8	78.7	97	10	T62112	T62112 yc66c02.r1
	18	11.8	78.7	99	12	AZ433742	AZ433742 1M0219H13
c	19	11.8	78.7	100	9	AA865812	AA865812 og97h05.s
c	20	11.4	76.0	22	12	AZ954618	AZ954618 2M0220E20
c	21	11.4	76.0	46	9	AA591686	AA591686 vl13g08.r
	22	11.4	76.0	50	9	AA108275	AA108275 EST0018 r
c	23	11.4	76.0	50	9	AU102591	AU102591 AU102591
c	24	11.4	76.0	50	9	AU102592	AU102592 AU102592
c	25	11.4	76.0	50	9	AU102593	AU102593 AU102593
c	26	11.4	76.0	50	9	AU102594	AU102594 AU102594
c	27	11.4	76.0	50	9	AU102595	AU102595 AU102595
c	28	11.4	76.0	50	9	AU107574	AU107574 AU107574
c	29	11.4	76.0	56	9	AI656187	AI656187 tt38f04.x
	30	11.4	76.0	68	10	T72238	T72238 yc68d01.r1
c	31	11.4	76.0	73	9	AA220616	AA220616 my25f09.r
c	32	11.4	76.0	74	10	BF528890	BF528890 602043353
	33	11.4	76.0	77	9	AA387938	AA387938 vc87h07.r
	34	11.4	76.0	77	10	T62949	T62949 yb99h02.s1
	35	11.4	76.0	85	9	AI167298	AI167298 ox65c07.s
	36	11.4	76.0	85	9	AA469098	AA469098 ne16g10.s
	37	11.4	76.0	85	9	AA529090	AA529090 vi32d12.r
	38	11.4	76.0	90	9	AA213781	AA213781 zr92g11.r
	39	11.4	76.0	91	9	AA089130	AA089130 mo21a01.r
c	40	11.4	76.0	97	12	AZ834937	AZ834937 2M0117G22
c	41	11.4	76.0	100	9	AW437175	AW437175 78050 MAR
	42	11.4	76.0	100	9	AW809349	AW809349 MR4-ST012
	43	11.4	76.0	100	10	BF807260	BF807260 IL0-CI019
c	44	11	73.3	31	9	AA981706	AA981706 ua25e05.r
	45	11	73.3	61	9	AI676111	AI676111 wc05e08.x

ALIGNMENTS

RESULT 1
BM023447/c
LOCUS BM023447 75 bp mRNA linear EST 30-OCT-2001
DEFINITION ie80e10.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION BM023447
VERSION BM023447.1 GI:16537803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 75)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T. , Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other_ESTs: ie80e10.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu)
Putative full length read
vector to vector length is 76.
FEATURES Location/Qualifiers
source 1. .75
/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
BASE COUNT 23 a 25 c 12 g 15 t
ORIGIN

Query Match 89.3%; Score 13.4; DB 10; Length 75;
Best Local Similarity 93.3%; Pred. No. 5.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 tccatggtgctcact 15
| ||||||||||||||
Db 50 TACATGGTGCTCACT 36

RESULT 2
AI022662
LOCUS AI022662 58 bp mRNA linear EST 18-JUN-1998
DEFINITION ox05h11.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655493 3' similar to SW:TCX1_HUMAN Q15763 T-COMPLEX TESTIS-SPECIFIC PROTEIN 1 HOMOLOG ;, mRNA sequence.
ACCESSION AI022662
VERSION AI022662.1 GI:3237903
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 58)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES Location/Qualifiers
source 1. .58
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1655493"
/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen 1NFLS library. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 14 a 18 c 8 g 17 t 1 others
ORIGIN

Query Match 82.7%; Score 12.4; DB 9; Length 58;
Best Local Similarity 92.9%; Pred. No. 1.7e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ccatggtgctcact 15
| ||||||||||||
Db 37 CAATGGTGCTCACT 50

RESULT 3
AL362924
LOCUS AL362924 74 bp mRNA linear EST 04-AUG-2000
DEFINITION AL362924 ICRFp 522 and 523 Mus musculus cDNA clone K9303B05 5', mRNA sequence.
ACCESSION AL362924
VERSION AL362924.1 GI:9692322
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 74)
AUTHORS Eickhoff,H., Schuchhardt,J., Ivanov,I., Meier-Ewert,S., O'Brien,J., Malik,A., Tandon,N., Wolski,E., Rohlfs,E., Nyarsik,L., Reinhardt,R., Nietfeld,W. and Lehrach,H.
TITLE Tissue gene expression analysis using arrayed normalized cDNA libraries
JOURNAL Genome Res. (2000) In press
COMMENT Contact: MPIMG
Abt.Lehrach
Max Planck Institut Fuer Molekulare Genetik
Ihnestrasse 73, Berlin, 14195 Germany
The cDNA libraries ICRFp 522 and 523 were normalized with oligonucleotide fingerprinting, resulting in a unique subset of 5376 cDNA clones.
FEATURES Location/Qualifiers
source 1. .74
/organism="Mus musculus"
/strain="Black 6"
/db_xref="taxon:10090"
/clone="K9303B05"
/clone_lib="ICRFp 522 and 523"
/tissue_type="embryo"
/dev_stage="9 and 12 pc embryo"
BASE COUNT 22 a 14 c 26 g 12 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 9; Length 74;
Best Local Similarity 92.9%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ccatggtgctcact 15
| ||||||||||||
Db 8 CCATGGTGCTCTCT 21

RESULT 4
W15664
LOCUS W15664 77 bp mRNA linear EST 10-SEP-1996
DEFINITION mb52d02.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:333027 5' similar to gb:V00714 Mouse gene for alpha-globin (MOUSE);, mRNA sequence.
ACCESSION W15664
VERSION W15664.1 GI:1290047

```
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 77)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:214427
            Seq primer: ETPrimer
            High quality sequence stop: 70.
FEATURES             Location/Qualifiers
     source          1. .77
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:333027"
                     /clone_lib="Soares mouse p3NMF19.5"
                     /dev_stage="19.5 dpc total fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCATTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library went through one round of
                     normalization to a Cot = 5. Library constructed by Bento
                     Soares and M.Fatima Bonaldo. RNA was kindly provided by
                     Dr. Minoru Ko (Wayne State University)."
BASE COUNT       23 a     15 c     28 g     11 t
ORIGIN


  Query Match             82.7%;  Score 12.4;  DB 10;  Length 77;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ccatggtgctcact 15
           ||||||||||| ||
Db      18 CCATGGTGCTCTCT 31


RESULT   5
AV832470/c
LOCUS       AV832470                 80 bp    mRNA    linear   EST 22-JUN-2001
DEFINITION  AV832470 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
            vulgare leaves vegetative stage Hordeum vulgare subsp. vulgare cDNA
            clone baak3f24, mRNA sequence.
ACCESSION   AV832470
VERSION     AV832470.1  GI:14524559
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 80)
  AUTHORS   Sato,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kazuhiro Sato
            Research Institute for Bioresources
            Okayama University, Barley Germplasm Center
            Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
            Email: kazsato@rib.okayama-u.ac.jp,
            URL:http://www.rib.okayama-u.ac.jp/barley/
            Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
            submission;
            database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES             Location/Qualifiers
     source          1. .80
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Akashinriki"
                     /db_xref="taxon:112509"
                     /clone="baak3f24"
                     /clone_lib="K. Sato unpublished cDNA library: Hordeum
                     vulgare subsp. vulgare leaves vegetative stage"
                     /tissue_type="leaves"
                     /dev_stage="vegetative stage"
BASE COUNT       25 a     13 c     22 g     14 t      6 others
ORIGIN


  Query Match             82.7%;  Score 12.4;  DB 9;  Length 80;
  Best Local Similarity   92.9%;  Pred. No. 1.9e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 ccatggtgctcact 15
           ||||||||||| ||
Db      14 CCATGGTGCTCTCT 1


RESULT   6
AZ648327/c
LOCUS       AZ648327                 62 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0517K13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0517K13 F, DNA sequence.
ACCESSION   AZ648327
VERSION     AZ648327.1  GI:11780683
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 62)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0517  row: K  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 62.
FEATURES             Location/Qualifiers
     source          1. .62
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0517K13"
```

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                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant; F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       11 a     20 c     15 g     16 t
ORIGIN


  Query Match             80.0%;  Score 12;  DB 12;  Length 62;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      2 ccatggtgctca 13
          ||||||||||||
Db     45 CCATGGTGCTCA 34


RESULT   7
TA138D06P
LOCUS       TA138D06P                 82 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 138d06, forward sequence,
            genomic survey sequence.
ACCESSION   AL465857
VERSION     AL465857.1  GI:11835283
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 82)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .82
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="138d06"
BASE COUNT       33 a     13 c     12 g     24 t
ORIGIN


  Query Match             80.0%;  Score 12;  DB 12;  Length 82;
  Best Local Similarity   100.0%;  Pred. No. 3e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      4 atggtgctcact 15
          ||||||||||||
Db     60 ATGGTGCTCACT 71


RESULT   8
AI930840/c
LOCUS       AI930840                  85 bp    mRNA    linear   EST 30-NOV-2001
DEFINITION  sb43a06.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1015-11 5' similar to TR:Q40290 Q40290 CAS15. [2] TR:Q40334 ;,
            mRNA sequence.
ACCESSION   AI930840
VERSION     AI930840.1  GI:5666804
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 85)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Trace considered overall poor quality
            Possible reversed clone: similarity on wrong strand This clone is
            available through: ResGen, Invitrogen Corp. 2130 South Memorial
            Parkway Huntsville, AL 35801 For further information call: (800
            )-533-4363 or contact via email: ccu@resgen.com
            Seq primer: -40RP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .85
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-11"
                     /clone_lib="Gm-c1015"
                     /tissue_type="Mature flowers, field grown plants"
                     /lab_host="XL10-Gold"
                     /note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
                     XhoI; This cDNA library was constructed from mRNA isolated
                     from mature flowers of field grown plants. The cDNA
                     library was prepared using the Stratagene pBluescript II
                     XR cDNA library construction kit. Complementary DNA was
                     synthesized from mRNA using a primer consisting of a poly
                     (dT) sequence with a XhoI restriction site. EcoRI adapters
                     were ligated to the blunt-ended cDNA fragments followed by
                     XhoI digestion. The cDNA fragments were directionally
                     cloned into the EcoRI-XhoI restriction site of the
                     pBluescript vector. The ligated cDNA fragments were
                     transformed into XL10-Gold host cells. This library was
                     constructed by Dr. Randy Shoemaker and Dr. John
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                    Erpelding."
BASE COUNT       25 a     15 c     25 g     20 t
ORIGIN


  Query Match             80.0%;  Score 12;  DB 9;  Length 85;
  Best Local Similarity   100.0%;  Pred. No. 3e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 catggtgctcac 14
          ||||||||||||
Db     83 CATGGTGCTCAC 72


RESULT   9
AA690354
LOCUS       AA690354                 90 bp    mRNA    linear   EST 16-DEC-1997
DEFINITION  vt31b01.r1 Barstead mouse proximal colon MPLRB6 Mus musculus cDNA
            clone IMAGE:1164649 5', mRNA sequence.
ACCESSION   AA690354
VERSION     AA690354.1  GI:2691290
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 90)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:630561
            Putative full length read
            vector to vector length is 147
            Seq primer: -28m13 rev2 ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .90
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1164649"
                     /clone_lib="Barstead mouse proximal colon MPLRB6"
                     /dev_stage="7 day juvenile"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACGAATCTGAAGTGGGAGCGGCCGCCCTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     [AATTCGGATCCTTG], digested with Not I and cloned into the
                     Not I and Eco RI sites of the modified pT7T3 vector.
                     Library constructed by Bob Barstead. "
BASE COUNT       26 a     26 c     16 g     22 t
ORIGIN


  Query Match             80.0%;  Score 12;  DB 9;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      3 catggtgctcac 14
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          ||||||||||||
Db     18 CATGGTGCTCAC 29


RESULT  10
AZ590927/c
LOCUS       AZ590927                 92 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0400G16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0400G16 R, DNA sequence.
ACCESSION   AZ590927
VERSION     AZ590927.1  GI:11713117
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0400  row: G  column: 16
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 92.
FEATURES             Location/Qualifiers
     source          1. .92
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0400G16"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       20 a     24 c     23 g     25 t
ORIGIN


  Query Match             80.0%;  Score 12;  DB 12;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 3.1e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      3 catggtgctcac 14
          ||||||||||||
Db     16 CATGGTGCTCAC 5


RESULT  11
TA358F01P/c
LOCUS       TA358F01P                 38 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 358f01, forward sequence,
            genomic survey sequence.
ACCESSION   AL494114
VERSION     AL494114.1  GI:11870743
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei.
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 38)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .38
                     /organism="Trypanosoma brucei"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="358f01"
BASE COUNT       16 a      5 c      6 g     11 t
ORIGIN


  Query Match             78.7%;  Score 11.8;  DB 12;  Length 38;
  Best Local Similarity   86.7%;  Pred. No. 2.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||||  ||| ||||
Db     30 TCCATGTTGCACACT 16


RESULT  12
AA285022
LOCUS       AA285022                  65 bp    mRNA    linear   EST 15-MAY-1997
DEFINITION  zt25e10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:714186 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS
            (HUMAN);, mRNA sequence.
ACCESSION   AA285022
VERSION     AA285022.1  GI:1927703
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 65)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -41m13 fwd. ET from Amersham.
FEATURES             Location/Qualifiers
     source          1. .65
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:714186"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT       7 a      21 c      17 g      20 t
ORIGIN


  Query Match             78.7%;  Score 11.8;  DB 9;  Length 65;
  Best Local Similarity   86.7%;  Pred. No. 3.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 tccatggtgctcact 15
          ||||  |||||||  ||
Db     23 TCCACGGTGCTCCCT 37


RESULT  13
AZ799758
LOCUS       AZ799758                  72 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0057G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0057G19 F, DNA sequence.
ACCESSION   AZ799758
VERSION     AZ799758.1  GI:12951196
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 72)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
```

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           Plate: 0057  row: G  column: 19
           Seq primer: CGTTGTAAAACGACGGCCAGT
           Class: plasmid ends
           High quality sequence stop: 72.
FEATURES             Location/Qualifiers
     source          1. .72
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0057G19"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT       13 a     18 c     16 g     25 t
ORIGIN


  Query Match             78.7%;  Score 11.8;  DB 12;  Length 72;
  Best Local Similarity   86.7%;  Pred. No. 3.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
           |||||| |||||| |
Db      48 TCCATGTTGCTCATT 62


RESULT 14
BI472373/c
LOCUS       BI472373                  89 bp    mRNA    linear   EST 24-AUG-2001
DEFINITION  fs02d01.y1 Zebrafish adult olfactory Danio rerio cDNA clone 5002416
            5', mRNA sequence.
ACCESSION   BI472373
VERSION     BI472373.1  GI:15288482
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 89)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de).
FEATURES             Location/Qualifiers
     source          1. .89
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5002416"
                     /clone_lib="Zebrafish adult olfactory"
                     /sex="mixed"
                     /tissue_type="Olfactory rosettes"
                     /dev_stage="adult"
                     /lab_host="D10Hb (Gibco BRL)"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
                     is a directionally cloned cDNA library from adult
                     Zebrafish olfactory epithelium."
BASE COUNT       26 a     21 c     25 g     17 t
ORIGIN


  Query Match             78.7%;  Score 11.8;  DB 10;  Length 89;
  Best Local Similarity   86.7%;  Pred. No. 3.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 tccatggtgctcact 15
           |||||||| ||| ||
Db      67 TCCATGGTTCTCTCT 53


RESULT 15
AV834264
LOCUS       AV834264                  91 bp    mRNA    linear   EST 22-JUN-2001
DEFINITION  AV834264 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
            vulgare shoots germination Hordeum vulgare subsp. vulgare cDNA
            clone rbags8j18, mRNA sequence.
ACCESSION   AV834264
VERSION     AV834264.1  GI:14526353
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. vulgare.
  ORGANISM  Hordeum vulgare subsp. vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 91)
  AUTHORS   Sato,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kazuhiro Sato
            Research Institute for Bioresources
            Okayama University, Barley Germplasm Center
            Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
            Email: kazsato@rib.okayama-u.ac.jp,
            URL:http://www.rib.okayama-u.ac.jp/barley/
            Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
            submission;
            database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES             Location/Qualifiers
     source          1. .91
                     /organism="Hordeum vulgare subsp. vulgare"
                     /cultivar="Haruna Nijo"
                     /db_xref="taxon:112509"
                     /clone="rbags8j18"
                     /clone_lib="K. Sato unpublished cDNA library: Hordeum
                     vulgare subsp. vulgare shoots germination"
                     /tissue_type="shoots"
                     /dev_stage="germination"
BASE COUNT       13 a     25 c     22 g     29 t      2 others
ORIGIN
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Query Match 78.7%; Score 11.8; DB 9; Length 91;
Best Local Similarity 86.7%; Pred. No. 3.9e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy       1 tccatggtgctcact 15
           ||| || ||||||||
Db      18 TCCGTGCTGCTCACT 32
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Search completed: July 21, 2002, 03:21:21
Job time: 16896 sec